

Search Notes

Application No.

09/843,221

Examiner

Christopher Nichols, Ph.D.

Applicant(s)

KOSTENUK ET AL.

Art Unit

1647

SEARCHED

Class	Subclass	Date	Examiner

INTERFERENCE SEARCHED

Class	Subclass	Date	Examiner

**SEARCH NOTES
(INCLUDING SEARCH STRATEGY)**

	DATE	EXMR
SEQ ID NO: 2	1/16/2004	CJN

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 16, 2004, 09:36:27 ; Search time 42 Seconds
(without alignments)
861.659 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1238	100.0	228	21	AAB16955	Human IgG1 Fc prot	
2	1238	100.0	228	21	AAY96529	Human IgG1 Fc chai	
3	1238	100.0	228	22	AAB98953	Human IgG1 Fc regi	
4	1238	100.0	228	23	AAU81074	Human IgG1 Fc. Ho	
5	1238	100.0	228	23	ABB73410	Human immunoglobul	
6	1238	100.0	228	23	AAE14310	Human immunoglobul	
7	1238	100.0	228	23	AAU73018	Human immunoglobul	
8	1238	100.0	228	23	AAG66012	Human immunoglobul	
9	1238	100.0	228	23	ABB04279	Human IgG1 Fc doma	
10	1238	100.0	228	24	ABJ38267	Human IgG1 Fc prot	
11	1238	100.0	243	21	AAB17957	Fc-MMP inhibitor f	
12	1238	100.0	243	23	ABB73425	Fc-MMP inhibitor f	
13	1238	100.0	247	21	AAB16958	Fc-TMP protein seq	
14	1238	100.0	247	23	ABB73411	Fc-TPO mimetic pep	
15	1238	100.0	248	21	AAB17951	Fc-TNF-alpha inhib	
16	1238	100.0	248	21	AAB17953	Fc-IL-1 antagonist	
17	1238	100.0	248	23	ABB73419	Fc-TNF-alpha inhib	
18	1238	100.0	248	23	ABB73421	Fc-interleukin 1 (
19	1238	100.0	252	21	AAB17955	Fc-VEGF antagonist	
20	1238	100.0	252	23	ABB73423	Fc-VEGF antagonist	
21	1238	100.0	253	21	AAB16964	Fc-EMP protein seq	
22	1238	100.0	253	23	ABB73415	Fc-EPO mimetic pep	
23	1238	100.0	268	21	AAB16959	Fc-TMP-TMP protein	
24	1238	100.0	268	23	ABB73412	Fc-TMP-TMP amino a	
25	1238	100.0	269	21	AAY96531	Human IgG1 Fc TMP	
26	1238	100.0	277	21	AAB16967	Fc-EMP-EMP protein	
27	1238	100.0	277	23	ABB73418	Fc-EMP-EMP nucleic	
28	1238	100.0	282	23	AAU81169	Echistatin/IgG Fc	
29	1238	100.0	374	19	AAW83963	Recombinant human	
30	1238	100.0	374	19	AAW49075	Recombinant human	
31	1238	100.0	401	22	AAY72922	Human met-Fc (lack	
32	1238	100.0	401	22	AAB80904	Human metFcdeltaC-	
33	1234	99.7	229	24	ABU07950	Human IgG Fc fragm	
34	1234	99.7	235	20	AAY01372	Amino acid sequenc	
35	1234	99.7	248	24	ABJ38332	TALL-1 inhibitory	
36	1234	99.7	248	24	ABJ38333	TALL-1 inhibitory	
37	1234	99.7	248	24	ABJ38334	TALL-1 inhibitory	
38	1234	99.7	252	24	ABJ38335	TALL-1 inhibitory	
39	1234	99.7	252	24	ABJ38336	TALL-1 inhibitory	
40	1234	99.7	252	24	ABJ38337	TALL-1 inhibitory	
41	1234	99.7	252	24	ABJ38338	TALL-1 inhibitory	
42	1234	99.7	252	24	ABJ38339	TALL-1 inhibitory	
43	1234	99.7	252	24	ABJ38340	TALL-1 inhibitory	
44	1234	99.7	252	24	ABJ38341	TALL-1 inhibitory	
45	1234	99.7	252	24	ABJ38342	TALL-1 inhibitory	

ALIGNMENTS

RESULT 1

AAB16955

ID AAB16955 standard; Protein; 228 AA.

XX

AC AAB16955;

XX

DT 31-OCT-2000 (first entry)

XX

DE Human IgG1 Fc protein sequence SEQ ID NO:2.

XX

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX

OS Homo sapiens.

XX

PN WO200024782-A2.

XX

PD 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US25044.

XX

PR 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheetham J, Boone TC;

XX

DR WPI; 2000-350702/30.

DR

N-PSDB; AAA69443.

XX

PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

XX

PS Claim 7; Page 176-177; 608pp; English.

XX

CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein

CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 2

AA96529

ID AAY96529 standard; Protein; 228 AA.

XX

AC AAY96529;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human IgG1 Fc chain.

XX

KW Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.

XX

OS Homo sapiens.

XX

PN WO200024770-A2.

XX

PD 04-MAY-2000.

XX

PF 22-OCT-1999; 99WO-US24834.

XX

PR 23-OCT-1998; 98US-0105348.

XX

PA (AMGE-) AMGEN INC.

XX

PI Liu C, Feige U, Cheetham J;

XX

DR WPI; 2000-365108/31.

DR N-PSDB; AAA29220.

XX
PT Thrombopoietic peptides which activate mpl receptors and increase the
PT production of platelets or platelet precursors, useful for treatment of
PT diseases which involve thombocytopenia
XX
PS Disclosure; Page 76-77; 9lpp; English.
XX
CC A compound which binds to an mpl receptor comprising a thrombopoietin
CC mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],
CC is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
CC 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2,
CC X_2-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and
CC X_1-X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A;
CC X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N,
CC or E; X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V,
CC L, F, S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K,
CC T, V, N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker
CC comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and
CC activate the c-Mpl receptor which mediates the activity of endogenous
CC thrombopoietin. The TMPs are useful for increasing the production of
CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
CC is useful for treatment of diseases which involve thombocytopenia, e.g.
CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
CC virus associated ITP, and systemic lupus erythematosus.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV	60
Db	1	MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV	60
Qy	61	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA	120
Db	61	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA	120
Qy	121	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	180
Db	121	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	180
Qy	181	SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	228
Db	181	SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	228

RESULT 3
AAB98953
ID AAB98953 standard; Protein; 228 AA.
XX
AC AAB98953;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human IgG1 Fc region.

XX
 KW Human; IgG1; immunoglobulin; Fc region; Fc fusion protein;
 KW misfolding; therapy; cancer; osteoarthritis; AIDS; obesity;
 KW inflammation; transplant rejection.
 XX
 OS Homo sapiens.
 XX
 PN WO200134638-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 10-NOV-2000; 2000WO-US30798.
 XX
 PR 12-NOV-1999; 99US-0165188.
 PR 09-NOV-2000; 2000US-0709704.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Treuheit MJ, O'Conner SR, Kosky AA;
 XX
 DR WPI; 2001-335908/35.
 DR N-PSDB; AAH25762.
 XX
 PT Correcting disulfide bond misfolds in Fc-containing proteins,
 PT particularly therapeutic Fc-containing fusion proteins or antibodies,
 PT by treatment with copper halide -
 XX
 PS Claim 30; Fig 5; 59pp; English.
 XX
 CC The present invention describes a process for preparing a
 CC pharmacologically active compound, involving preparing a compound
 CC comprising an immunoglobulin Fc domain fused to a protein of interest,
 CC treating the compound with a copper(II) halide and isolating the treated
 CC molecule. This can be used to correct misfolding of Fc domain containing
 CC proteins, for use in therapeutic agents which may be used in the
 CC treatment of cancer, inflammation, transplant rejection, AIDS,
 CC osteoarthritis and obesity. The present sequence is the IgG1 Fc domain.
 XX
 SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 22; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.2e-91;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

Db

|||||
181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 4

AAU81074

ID AAU81074 standard; Protein; 228 AA.

XX

AC AAU81074;

XX

DT 09-APR-2002 (first entry)

XX

DE Human IgG1 Fc.

XX

KW Human; IgG Fc; anticoagulant; thrombolytic; cytostatic;

KW antiinflammatory; immunosuppressive; osteopathic; antagonist;

KW laminin; saw-scaled viper; echistatin; integrin; selectin; vinculin;

KW platelet aggregation; angiogenesis; tumour; inflammation;

KW autoimmune disease; rheumatoid arthritis; osteoporosis.

XX

OS Homo sapiens.

XX

PN WO200181377-A2.

XX

PD 01-NOV-2001.

XX

PF 23-APR-2001; 2001WO-US13069.

XX

PR 21-APR-2000; 2000US-198919P.

PR 03-MAY-2000; 2000US-201394P.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Kohno T, Lacey DL, Boone TC;

XX

DR WPI; 2002-062025/08.

DR N-PSDB; ABK24097.

XX

PT Composition comprising integrin or adhesion antagonistic peptide and

PT vehicle, useful for treating or preventing platelet aggregation, has a

PT longer half-life than free peptide -

XX

PS Claim 9; Fig 3; 68pp; English.

XX

CC The invention relates to a composition comprising an integrin/adhesion

CC antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides

CC are based on laminin or saw-scaled viper echistatin and target integrin,

CC selectin or vinculin. Also included are compounds of formula (Ia) and

CC their multimers $(X^1)_a - F^1 - (X^2)_b$ where;

CC F^1 = Fc domain;

CC X^1 and X^2 = $-(L^1)_c - P^1$, $(L^1)_c - P^1 - (L^2)_d - P^2$,

CC $(L^1)_c - P^1 - (L^2)_d - P^2 - (L^3)_e - P^3$ or

CC $(L^1)_c - P^1 - (L^2)_d - P^2 - (L^3)_e - P^3 - (L^4)_f - P^4$;

CC $P^1 - P^4$ = same or different (I);

CC $L^1 - L^4$ = same or different linkers;

CC a-f = 0 or 1, provided at least one of a and b = 1,

CC a nucleic acid that encodes (Ia), an expression vector containing the

CC nucleic acid, host cells containing the vector, producing a
CC pharmaceutically active compound (B) by covalently linking at least one
CC Fc domain to at least one amino acid sequence of a selected randomized
CC (I) and any of six laminin-related peptides (Ib). The compositions are
CC used prophylactically and therapeutically in the same way as (I), e.g. to
CC inhibit platelet aggregation or angiogenesis (tumours), or to treat
CC inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many
CC different forms of osteoporosis, also for diagnosis. Attaching the
CC vehicle (especially Fc domain) to (I) increases the half-life (free (I)
CC are normally degraded very quickly in vivo). The present sequence
CC is human IgG1 Fc which is used as a vehicle for the antagonists of
CC the invention.

XX

SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
          ||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 5

ABB73410

ID ABB73410 standard; Protein; 228 AA.

XX

AC ABB73410;

XX

DT 05-APR-2002 (first entry)

XX

DE Human immunoglobulin G1 Fc (IgG1 Fc) amino acid SEQ ID NO:2.

XX

KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;

KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;

KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;

KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;

KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;

KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;

KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;

KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;

KW sleep disorder; neurological degenerative disease; anaemia;

KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;

KW Fanconi's syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200183525-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14310.
 XX
 PR 03-MAY-2000; 2000US-0563286.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX
 DR WPI; 2002-130313/17.
 DR N-PSDB; ABL35760.
 XX
 PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX
 PS Claim 7; Fig 4; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.2e-91;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPVETCVVVDVSHEDPEVKFNWYV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPVETCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228

RESULT 6

AAE14310

ID AAE14310 standard; Protein; 228 AA.

XX

AC AAE14310;

XX

DT 07-MAR-2002 (first entry)

XX

DE Human immunoglobulin G (IgG1) Fc.

XX

KW Human; calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;
 KW immunoglobulin G; IgG; osteopathic.

XX

OS Homo sapiens.

XX

PN WO200183526-A2.

XX

PD 08-NOV-2001.

XX

PF 03-MAY-2001; 2001WO-US14320.

XX

PR 03-MAY-2000; 2000US-201511P.

PR 02-MAY-2001; 2001US-0847712.

XX

PA (AMGE-) AMGEN INC.

XX

PI Liu C, Marshall WS, Reynolds A;

XX

DR WPI; 2002-034503/04.

DR N-PSDB; AAD23840.

XX

PT Compositions comprising Calcitonin receptor modulator domains, useful
 PT for treating osteoporosis -

XX

PS Claim 8; Fig 3; 64pp; English.

XX

CC The invention relates to therapeutic agents that modulate the
 CC activity of calcitonin (CT) receptor. Modulators of CT receptor
 CC comprise a CT receptor modulating domain and a vehicle such as a
 CC polymer or an Fc domain, where the vehicle is covalently attached
 CC to the CT receptor modulating domain. The compositions comprising
 CC CT receptor modulating domains are used to treat osteoporosis.
 CC The present sequence is human immunoglobulin G (IgG1) Fc protein

CC used in the invention.

XX

SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 7

AAU73018

ID AAU73018 standard; Protein; 228 AA.

XX

AC AAU73018;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human immunoglobulin G (IgG) Fc region.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.


```

XX      (AMGE-) AMGEN INC.
XX
PI      Kostenuik P,  Liu C,  Lacey DL;
XX
DR      WPI; 2002-066435/09.
DR      N-PSDB; AAS97392.
XX
PT      Composition, useful for treating osteopenia, comprises parathyroid
PT      hormone and parathyroid hormone-related protein receptor modulators -
XX
PS      Claim 6; Figure 3; 107pp; English.
XX
CC      The invention relates to a composition (I) comprising modulators of
CC      parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC      which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC      comprising PTH agonist optionally with a bone resorption inhibitor, such
CC      as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC      oestrogens, oestrogen receptor modulators and tibolone is useful for
CC      treating osteopenia. (I) is useful for therapeutic and prophylactic
CC      purposes. Antagonists of PTH receptor are useful in treating primary and
CC      secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC      particularly breast and prostate cancer, cachexia and anorexia,
CC      osteopenia, including various forms of osteoporosis, Paget's disease of
CC      bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC      traumatic injury or nontraumatic necrosis associated with Gaucher's
CC      disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC      arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC      useful as therapeutic agents in conditions including fracture repair
CC      (including healing of non-union fractures), osteopenia, including various
CC      forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC      and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC      related amino acid sequences of the invention.
XX
SQ      Sequence      228 AA;

Query Match          100.0%;  Score 1238;  DB 23;  Length 228;
Best Local Similarity 100.0%;  Pred. No. 1.2e-91;
Matches 228;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV  60

Qy      61  DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy      121  KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      : 121  KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy      181  SDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  SDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

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AAG66012

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DR

PT

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1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDILMI SRTPEVTCVVVDVSHEDPEVKFNWYV 60
 |||||
 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDILMI SRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy	61	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK	120
Db	61	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK	120
Qy	121	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	180
Db	121	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	180
Qy	181	SDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK	228
Db	181	SDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK	228

RESULT 9

ABB04279

ID ABB04279 standard; Protein; 228 AA.

XX

AC ABB04279;

XX

DT 13-FEB-2002 (first entry)

XX

DE Human IgG1 Fc domain.

XX

KW Glucagon antagonist; antidiabetic; anti-hormonal; Fc domain;

KW non-insulin dependent diabetes mellitus; human; immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200183527-A2.

XX

PD 08-NOV-2001.

XX

PF 03-MAY-2001; 2001WO-US14321.

XX

PR 03-MAY-2000; 2000US-201436P.

PR 02-MAY-2001; 2001US-0847249.

XX

PA (AMGE-) AMGEN INC.

XX

PI Marshall WS, Stark KL;

XX

DR WPI; 2002-017738/02.

DR N-PSDB; ABA03672.

XX

PT Compositions comprising glucagon antagonist domains, useful for
PT treating diabetes mellitus -

XX

PS Claim 8; Fig 2; 54pp; English.

XX

CC The invention relates to compositions comprising a glucagon antagonist
CC domain and a vehicle, such as a polymer (e.g. PEG or dextran) or,
CC preferably, an Fc domain. The vehicle is covalently attached to the
CC glucagon antagonist domain. The compositions are administered to
CC treat non-insulin dependent diabetes mellitus. The present sequence
CC is the human IgG Fc domain, which may be used as the vehicle
CC in the compositions of the invention.

XX

SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 23; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 10

ABJ38267

ID ABJ38267 standard; Protein; 228 AA.

XX

AC ABJ38267;

XX

DT 12-JUN-2003 (first entry)

XX

DE Human IgG1 Fc protein SEQ ID No 2.

XX

KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
KW gene therapy; human IgG1Fc; human.

XX

OS Homo sapiens.

XX

PN WO200292620-A2.

XX

PD 21-NOV-2002.

XX

PF 13-MAY-2002; 2002WO-US15273.

XX

PR 11-MAY-2001; 2001US-290196P.

XX

PA (AMGE-) AMGEN INC.

XX

PI Min H, Hsu H;

XX

DR WPI; 2003-156719/15.

DR N-PSDB; ABT33856.

XX
PT New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas -
XX
PS Claim 36; Fig 3; 236pp; English.
XX
CC The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
CC lymphoma. The composition may also be used in treating inflammations
CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
CC and vasculitis. Disorders may be treated with the novel composition using
CC gene therapy. This sequence represents a human IgG1Fc protein relating to
CC the TALL-1 sequence of the invention.
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 24; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228

RESULT 11

AAB17957

ID AAB17957 standard; Protein; 243 AA.

XX

AC AAB17957;

XX

DT 31-OCT-2000 (first entry)

XX

DE Fc-MMP inhibitor fusion protein sequence SEQ ID NO:1068.

XX

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;

KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;

KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 12

ABB73425

ID ABB73425 standard; Protein; 243 AA.

XX

AC ABB73425;

XX

DT 05-APR-2002 (first entry)

XX

DE Fc-MMP inhibitor fusion nucleic acid SEQ ID NO:1067.

XX

KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200183525-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14310.

XX

PR 03-MAY-2000; 2000US-0563286.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX

DR WPI; 2002-130313/17.

DR N-PSDB; ABL35775.

XX

PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,

PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX

PS Example 7; Fig 25A-B; 176pp; English.

XX

CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 23; Length 243;

Best Local Similarity 100.0%; Pred. No. 1.3e-91;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYV 60
          |||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVSVLTVHLQDNLGKEYKCKVSNKALPAPIEKTISKA 120
          |||
Db     61 DGVEVHNAKTKPREEQYNSTYRVSVLTVHLQDNLGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
          |||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
          |||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 13

AAB16958

ID AAB16958 standard; Protein; 247 AA.

XX

AC AAB16958;

XX

DT 31-OCT-2000 (first entry)

XX
 DE Fc-TMP protein sequence SEQ ID NO:6.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 DR N-PSDB; AAA69444.
 XX
 PT Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 21; Page 179-180; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1238; DB 21; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.3e-91;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
        |||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        |||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        |||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
        |||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

```

RESULT 14

ABB73411

ID ABB73411 standard; Protein; 247 AA.

XX

AC ABB73411;

XX

DT 05-APR-2002 (first entry)

XX

DE Fc-TPO mimetic peptide (Fc-TMP) amino acid SEQ ID NO:6.

XX

KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200183525-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14310.

XX

PR 03-MAY-2000; 2000US-0563286.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX

DR WPI; 2002-130313/17.

DR N-PSDB; ABL35761.

XX

PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX

PS Claim 21; Fig 7; 176pp; English.

XX

CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1238; DB 23; Length 247;

Best Local Similarity 100.0%; Pred. No. 1.3e-91;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK 228

Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK 228

RESULT 15

AAB17951

ID AAB17951 standard; Protein; 248 AA.

XX

AC AAB17951;

XX

DT 31-OCT-2000 (first entry)

XX

DE Fc-TNF-alpha inhibitor fusion protein sequence SEQ ID NO:1056.

XX

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX

OS Synthetic.

XX

PN WO200024782-A2.

XX

PD 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US25044.

XX

PR 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheetham J, Boone TC;

XX

DR WPI; 2000-350702/30.

DR N-PSDB; AAA69501.

XX

PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

XX

PS Example 4; Page 568-569; 608pp; English.

XX

CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein

CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 248 AA;

Query Match 100.0%; Score 1238; DB 21; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 228
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 228
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Search completed: January 16, 2004, 09:37:55

Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 16, 2004, 09:36:27 ; Search time 21 Seconds
(without alignments)
459.375 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1234	99.7	229	4	US-09-122-144-2
2	1234	99.7	347	1	US-07-940-861-43
3	1234	99.7	347	1	US-08-459-512-43
4	1234	99.7	347	2	US-08-459-657-43
5	1234	99.7	347	2	US-08-460-132-43
6	1234	99.7	347	3	US-08-466-465-8
7	1234	99.7	347	5	PCT-US92-02050-43
8	1234	99.7	446	4	US-09-157-452B-12
9	1234	99.7	482	4	US-09-189-129-2
10	1233	99.6	232	2	US-08-595-043A-50
11	1233	99.6	235	3	US-09-131-247-6

12	1233	99.6	331	3	US-09-178-869-2	Sequence 2, Appli
13	1233	99.6	331	4	US-09-761-413-2	Sequence 2, Appli
14	1233	99.6	360	4	US-09-180-100-11	Sequence 11, Appl
15	1233	99.6	371	1	US-08-236-311-7	Sequence 7, Appli
16	1233	99.6	371	3	US-08-457-918-7	Sequence 7, Appli
17	1233	99.6	376	4	US-09-180-100-22	Sequence 22, Appl
18	1233	99.6	387	1	US-08-470-299-4	Sequence 4, Appli
19	1233	99.6	388	3	US-09-131-247-16	Sequence 16, Appl
20	1233	99.6	389	3	US-09-131-247-14	Sequence 14, Appl
21	1233	99.6	396	2	US-08-784-512-3	Sequence 3, Appli
22	1233	99.6	396	3	US-09-176-228-3	Sequence 3, Appli
23	1233	99.6	424	4	US-09-333-593A-8	Sequence 8, Appli
24	1233	99.6	424	5	PCT-US95-03866-12	Sequence 12, Appl
25	1233	99.6	424	5	PCT-US95-03866-14	Sequence 14, Appl
26	1233	99.6	437	5	PCT-US96-10043-11	Sequence 11, Appl
27	1233	99.6	442	5	PCT-US96-10043-9	Sequence 9, Appli
28	1233	99.6	446	3	US-08-397-411-7	Sequence 7, Appli
29	1233	99.6	449	1	US-08-458-516-13	Sequence 13, Appl
30	1233	99.6	459	1	US-08-157-101A-7	Sequence 7, Appli
31	1233	99.6	475	4	US-09-740-002-27	Sequence 27, Appl
32	1233	99.6	476	2	US-08-378-939-10	Sequence 10, Appl
33	1233	99.6	476	3	US-08-487-550-4	Sequence 4, Appli
34	1233	99.6	476	3	US-08-487-550-12	Sequence 12, Appl
35	1233	99.6	476	4	US-09-526-098-4	Sequence 4, Appli
36	1233	99.6	476	4	US-09-526-098-12	Sequence 12, Appl
37	1233	99.6	478	3	US-08-487-550-8	Sequence 8, Appli
38	1233	99.6	478	4	US-09-526-098-8	Sequence 8, Appli
39	1233	99.6	488	3	US-08-776-511-2	Sequence 2, Appli
40	1233	99.6	592	4	US-09-313-942-8	Sequence 8, Appli
41	1233	99.6	680	3	US-08-227-496C-15	Sequence 15, Appl
42	1233	99.6	691	4	US-09-313-942-20	Sequence 20, Appl
43	1233	99.6	694	4	US-09-313-942-22	Sequence 22, Appl
44	1233	99.6	859	4	US-09-313-942-7	Sequence 7, Appli
45	1233	99.6	951	4	US-09-313-942-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-122-144-2

; Sequence 2, Application US/09122144A

; Patent No. 6485726

; GENERAL INFORMATION:

; APPLICANT: Blumberg, Richard S.

; APPLICANT: Simister, Neil E.

; APPLICANT: Lencer, Wayne I.

; TITLE OF INVENTION: RECEPTOR SPECIFIC TRANSEPITHELIAL TRANSPORT OF THERAPEUTICS

; FILE REFERENCE: S1383/7003

; CURRENT APPLICATION NUMBER: US/09/122,144A

; CURRENT FILING DATE: 1998-07-24

; EARLIER APPLICATION NUMBER: US 09/122,144

; EARLIER FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 22

; SEQ ID NO 2

; LENGTH: 229

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-144-2

Query Match 99.7%; Score 1234; DB 4; Length 229;
Best Local Similarity 99.6%; Pred. No. 3.5e-117;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
      : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 61

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
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Db     62 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 121

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
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Db    122 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
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RESULT 2

US-07-940-861-43

; Sequence 43, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-940-861-43

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Query Match          99.7%; Score 1234; DB 1; Length 347;
Best Local Similarity 99.6%; Pred. No. 6.3e-117;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
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Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
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RESULT 3

US-08-459-512-43

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; Sequence 43, Application US/08459512
; Patent No. 5728677
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue

```

```

;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022-6250
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,512
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/02050
;      FILING DATE:  12-MAR-1992
;      APPLICATION NUMBER:  US 07/667,971
;      FILING DATE:  12-MAR-1991
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/770,967
;      FILING DATE:  07-OCT-1991
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY, James F., Jr.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B151CIP2
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)715-0600
;      TELEFAX:  (212)715-0673
;      TELEX:  14-8367
;      INFORMATION FOR SEQ ID NO:  43:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  347 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-459-512-43

```

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Query Match          99.7%;  Score 1234;  DB 1;  Length 347;
Best Local Similarity 99.6%;  Pred. No. 6.3e-117;
Matches 227;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
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Db      180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
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Db      240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy      181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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Db      300 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347

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RESULT 4

US-08-459-657-43

; Sequence 43, Application US/08459657
; Patent No. 5914111
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,657
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-459-657-43

Query Match 99.7%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 6.3e-117;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
: |||||
Db 120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
: |||||
Db 180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
: |||||
Db 240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
: |||||
Db 300 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 347

RESULT 5

US-08-460-132-43

; Sequence 43, Application US/08460132

; Patent No. 5928643

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; APPLICANT: WALLNER, Barbara P.

; APPLICANT: MILLER, Glenn T.

; APPLICANT: ROSA, Margaret D.

; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE

; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 875 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022-6250

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,132

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/940,861

; FILING DATE: 21-OCT-1992

; APPLICATION NUMBER: PCT/US92/02050

; FILING DATE: 12-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/667,971

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/770,967

; FILING DATE: 07-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-132-43

Query Match 99.7%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 6.3e-117;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
      : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

QY      61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
      : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

QY      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
      : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

QY      181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      300 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 347
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RESULT 6

US-08-466-465-8

; Sequence 8, Application US/08466465
; Patent No. 6162432

; GENERAL INFORMATION:

; APPLICANT: Wallner, Barbara P.
; APPLICANT: Cooper, Kevin D.
; TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
; TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using
; TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/466,465
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/08755
;   FILING DATE:  06-OCT-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/862,022
;   FILING DATE:  12-APR-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/770,969
;   FILING DATE:  07-OCT-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Myers, Louis (PLM)
;   REGISTRATION NUMBER:  35,965
;   REFERENCE/DOCKET NUMBER:  BGP-111CP
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617)227-7400
;   TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  347 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-466-465-8

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Query Match          99.7%;  Score 1234;  DB 3;  Length 347;
Best Local Similarity 99.6%;  Pred. No. 6.3e-117;
Matches 227;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
      : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 VDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 179

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy     121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 299

Qy     181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 347

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RESULT 7

PCT-US92-02050-43

```

; Sequence 43, Application PC/TUS9202050
; GENERAL INFORMATION:
;   APPLICANT:  BIOGEN, INC.
;   APPLICANT:  WALLNER, Barbara P.
;   APPLICANT:  MILLER, Glenn T.

```

```

; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 19920312
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 715-0600
; TELEFAX: (212) 715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02050-43

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```

Query Match          99.7%; Score 1234; DB 5; Length 347;
Best Local Similarity 99.6%; Pred. No. 6.3e-117;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        : ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      120 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 179

Qy      61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      180 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 239

Qy      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 299

```


US-09-189-129-2

; Sequence 2, Application US/09189129
; Patent No. 6323027
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; APPLICANT: Benjamin, Christopher D
; APPLICANT: Hession, Catherine A
; APPLICANT: Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,129
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: A006 PCT CIP
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL: YES
; ANTI-SENSE: NO

US-09-189-129-2

Query Match 99.7%; Score 1234; DB 4; Length 482;
Best Local Similarity 99.6%; Pred. No. 1e-116;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
: ||||||||||||||||||||||||||||||||||||||||||||
Db 255 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 314
Qy 61 DGVEVHNAKTKPREEQYNSTYRVSVLTVQLHQLDNLGKEYKCKVSNKALPAPIEKTISKA 120

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Db      315 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 374
Qy      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db      375 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 434
Qy      181 SDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db      435 SDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 482

```

RESULT 10

US-08-595-043A-50

```

; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
;   APPLICANT: SGARLATO, GREGORY D.
;   TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
;   NUMBER OF SEQUENCES: 90
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: MEDLEN & CARROLL
;     STREET: 220 MONTGOMERY STREET, SUITE 2200
;     CITY: SAN FRANCISCO
;     STATE: CALIFORNIA
;     COUNTRY: UNITED STATES OF AMERICA
;     ZIP: 94104
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/595,043A
;     FILING DATE: 31-JAN-1996
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: CARROLL, PETER G.
;     REGISTRATION NUMBER: 32,837
;     REFERENCE/DOCKET NUMBER: SGAR-00371
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 705-8410
;     TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 232 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein

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US-08-595-043A-50

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Query Match          99.6%; Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.5e-117;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
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Db	6	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD	65
Qy	62	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121
Db	66	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	125
Qy	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	181
Db	126	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	185
Qy	182	DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK	228
Db	186	DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK	232

RESULT 11

US-09-131-247-6

```

; Sequence 6, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Hershenson, Susan
; APPLICANT: Bevilacqua, Michael P.
; APPLICANT: Collins, David S.
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
US-09-131-247-6

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Query Match 99.6%; Score 1233; DB 3; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.6e-117;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD	61
Db	9	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD	68
Qy	62	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121
Db	69	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	128
Qy	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	181
Db	129	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	188

Qy 182 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
 |||
 Db 189 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 235

RESULT 12

US-09-178-869-2

; Sequence 2, Application US/09178869B

; Patent No. 6197294

; GENERAL INFORMATION:

APPLICANT: Tao, Weng

; APPLICANT: Wong, Shou

; APPLICANT: Hickey, William F

; APPLICANT: Hammang, Joseph P.

; APPLICANT: Baetge, E. Edward

; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION

; FILE REFERENCE: 17810-043

; CURRENT APPLICATION NUMBER: US/09/178,869B

; CURRENT FILING DATE: 1998-10-26

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 331

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; TYPE: PRT
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; ORGANISM: Homo sapiens

US-09-178-869-2

Query Match 99.6%; Score 1233; DB 3; Length 331;

Best Local Similarity 100.0%; Pred. No. 7.5e-117;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db 105 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD 164

Qy 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
| | | | |

Db 165 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 224

[illegible]

Db 225 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLD 284

Qy 182 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228

Db 285 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 331

RESULT 13

US-09-761-413-2

; Sequence 2, Application US/09761413

; Patent No. 6506891

; GENERAL INFORMATION:

; APPLICANT: Tao, Weng

; APPLICANT: Wong, Shou

; APPLICANT: Hickey, William F

APPLICANT: Hammang, Joseph P.

```
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-413-2
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Query Match          99.6%; Score 1233; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 7.5e-117;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
          |||
Db      105 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 164

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
          |||
Db      165 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 224

Qy      122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
          |||
Db      225 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 284

Qy      182 DGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK 228
          |||
Db      285 DGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK 331
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RESULT 14

```
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11
```

Query Match 99.6%; Score 1233; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.4e-117;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 193

Qy     62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 253

Qy    122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 313

Qy    182 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK 228
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK 360
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RESULT 15

US-08-236-311-7

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; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
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; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-236-311-7

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Query Match          99.6%; Score 1233; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 8.8e-117;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      145 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 204

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      205 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 264

Qy      122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      265 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 324

Qy      182 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||
Db      325 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 371

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Search completed: January 16, 2004, 09:39:18
Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 16, 2004, 09:36:27 ; Search time 21 Seconds
(without alignments)
1044.117 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1233	99.6	255	4	S31866	Ig gamma-1 chain C
2	1233	99.6	330	1	GHHU	Ig gamma-1 chain C
3	1227	99.1	374	2	S69339	Ig heavy chain V r
4	1180	95.3	234	2	PT0207	Ig gamma chain C r
5	1146	92.6	377	2	A23511	Ig gamma-3 chain C
6	1144	92.4	377	2	A60764	Ig gamma-3 chain C
7	1142.5	92.3	326	1	G2HU	Ig gamma-2 chain C
8	1135	91.7	327	1	G4HU	Ig gamma-4 chain C
9	1121	90.5	289	1	G3HUWI	Ig gamma-3 heavy c
10	918.5	74.2	323	1	GHRB	Ig gamma chain C r
11	906.5	73.2	328	2	I47160	Ig gamma 2b chain
12	906.5	73.2	328	2	I47159	Ig gamma 2a chain
13	903.5	73.0	277	2	I47162	Ig gamma 4 chain c

14	889	71.8	329	1	G2GP	Ig gamma-2 chain C
15	885.5	71.5	328	2	I47158	Ig gamma 1 chain c
16	878.5	71.0	328	2	I47161	Ig gamma 3 chain c
17	855.5	69.1	470	2	S22080	Ig heavy chain pre
18	846	68.3	308	2	C30554	Ig heavy chain C r
19	846	68.3	472	2	S31459	Ig gamma-1 chain -
20	845.5	68.3	329	1	G3MSC	Ig gamma-3 chain C
21	838	67.7	333	2	PS0018	Ig gamma-2b chain
22	834.5	67.4	398	1	G3MSM	Ig gamma-3 chain C
23	827.5	66.8	444	2	PC4436	monoclonal antibod
24	818.5	66.1	326	2	PS0017	Ig gamma-1 chain C
25	817.5	66.0	324	1	G1MS	Ig gamma-1 chain C
26	812.5	65.6	393	1	G1MSM	Ig gamma-1 chain C
27	809.5	65.4	329	2	S00847	Ig gamma-2c chain
28	809	65.3	330	1	G2MSA	Ig gamma-2a chain
29	809	65.3	469	2	S37483	Ig gamma-2a chain
30	804	64.9	399	1	G2MSAM	Ig gamma-2a chain
31	802	64.8	335	1	G2MSAB	Ig gamma-2a chain
32	794	64.1	446	2	S40295	Ig gamma-2a chain
33	785.5	63.4	322	2	PS0019	Ig gamma-2a chain
34	779	62.9	474	1	G2MS11	Ig gamma-2b chain
35	774	62.5	405	1	G2MSBM	Ig gamma-2b chain
36	764	61.7	327	2	S06611	Ig gamma-2 chain C
37	757	61.1	475	2	S01321	Ig gamma-2b chain
38	707	57.1	180	2	I46732	Ig gamma heavy cha
39	577.5	46.6	249	2	S69340	Ig heavy chain VHI
40	574.5	46.4	218	2	A36040	Ig heavy chain V-I
41	571	46.1	152	2	S14236	Ig gamma-1 chain C
42	395.5	31.9	572	2	B46529	Ig Y heavy chain (
43	358	28.9	343	2	S25644	Ig mu chain C regi
44	358	28.9	453	2	S37768	Ig mu chain C regi
45	357.5	28.9	549	2	S04845	Ig heavy chain pre

ALIGNMENTS

RESULT 1

S31866

Ig gamma-1 chain C region - synthetic

C;Species: synthetic

A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C;Accession: S31866

R;Filpula, D.

submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene products.

A;Reference number: S31866

A;Accession: S31866

A;Molecule type: mRNA

A;Residues: 1-255 <FIL>

A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C;Keywords: immunoglobulin

F;1-22/Region: Escherichia coli outer membrane protein A precursor

F;23-255/Region: human Ig gamma-1 chain C region

Query Match 99.6%; Score 1233; DB 4; Length 255;
 Best Local Similarity 100.0%; Pred. No. 6.8e-89;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
          |||
Db      29 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 88

Qy     62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
          |||
Db     89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148

Qy    122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
          |||
Db    149 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 208

Qy    182 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK 228
          |||
Db    209 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK 255
  
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RESULT 2

GHHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, 239-Asp and 241-Leu

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.;
 Edelman, G.M.

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H-1-H-4.
 A;Reference number: A90563; MUID:71064024; PMID:5489771
 A;Contents: myeloma protein Eu
 A;Accession: B90563
 A;Molecule type: protein
 A;Residues: 1-96,'R',98-135 <CUN>
 A;Note: this sequence has the Glm(3) marker, 97-Arg
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence of heavy-chain cyanogen bromide fragments H-5-H-7.
 A;Reference number: A90564; MUID:71064025; PMID:5530842
 A;Contents: Eu
 A;Accession: A90564
 A;Molecule type: protein
 A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'M',242-267,'DGEPE',273-329 <RUT>
 A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
 R;Ponstingl, H.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), III. Die chymotryptischen Peptide der H-Kette, Anordnung der tryptischen Peptide und Diskussion der vollstaendigen Primaerstruktur.
 A;Reference number: A91668; MUID:77070269; PMID:826475
 A;Contents: myeloma protein Nie
 A;Accession: B91668
 A;Molecule type: protein
 A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',270-271,'D',273-330 <PON>
 A;Note: this sequence has the Glm(17) and Glm(1) markers
 R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
 A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL, I.
 A;Reference number: A91723; MUID:83289131; PMID:6884994
 A;Contents: myeloma protein KOL; disulfide bonds
 A;Accession: A91723
 A;Molecule type: protein
 A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH>
 A;Note: this sequence has the Glm(3) and Glm(non-1) markers
 R;Gall, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide bonds.
 A;Reference number: A90565; MUID:71064027; PMID:4923144
 A;Contents: annotation; disulfide bonds
 R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
 A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains the cyanogenbromide cleavage products, and the disulfide bridges.
 A;Reference number: A91667; MUID:77070267; PMID:1002129
 A;Contents: annotation; disulfide bonds

C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.6%; Score 1233; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 9.4e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
      |||
Db     104 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 163

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      |||
Db     164 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

Qy     122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
      |||
Db     224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 283

Qy     182 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 228
      |||
Db     284 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 330

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RESULT 3

S69339

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C;Accession: S69339; S72664

R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A;Reference number: S69339; MUID:95262687; PMID:7744049

A;Accession: S69339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <KHA>

A;Cross-references: EMBL:X81695

R;Khamlichi, A.A.

submitted to the EMBL Data Library, September 1994

A;Reference number: S72664

A;Accession: S72664

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140,'C',142-374 <KH2>

A;Cross-references: EMBL:X81695

C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 99.1%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 3.2e-88;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
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Db     148 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 207

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      |||
Db     208 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267

Qy     122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
      |||
Db     268 GQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 327

Qy     182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
      |||
Db     328 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
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RESULT 4

PT0207

Ig gamma chain C region - chimpanzee

C;Species: Pan troglodytes (chimpanzee)

C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999

C;Accession: PT0207

R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.

Mol. Immunol. 28, 319-322, 1991

A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.

A;Reference number: PT0207; MUID:91287716; PMID:2062315

A;Accession: PT0207

A;Molecule type: mRNA

A;Residues: 1-234 <EHR>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 95.3%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 8.2e-85;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
      |
Db     15 DTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      |||
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```

Db          75 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134
Qy          122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
          |||
Db          135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLD 194
Qy          182 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKS 221
          |||
Db          195 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKS 234

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RESULT 5

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999

C;Accession: A23511

R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: comparison with the other human C-gamma genes.

A;Reference number: A23511; MUID:86148507; PMID:3081877

A;Accession: A23511

A;Molecule type: DNA

A;Residues: 1-377 <HUC>

A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1;

PID:g577056

C;Genetics:

A;Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

A;Map position: 14q32.33-14q32.33

A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

```

Query Match          92.6%;  Score 1146;  DB 2;  Length 377;
Best Local Similarity 92.5%;  Pred. No. 6.7e-82;
Matches 210;  Conservative 8;  Mismatches 9;  Indels 0;  Gaps 0;

```

```

Qy          2 DKTHTCPPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
          |
Db          151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210
Qy          62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
          |||
Db          211 GVEVHNAKTKPREEQYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
Qy          122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
          |||
Db          271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330
Qy          182 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
          |||
Db          331 DGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRFQKSLSLSPGK 377

```

RESULT 6

A60764

Ig gamma-3 chain C region, form LAT - human

C;Species: Homo sapiens (man)

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999

C;Accession: A60764

R;Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converted region and three hinge exons.

A;Reference number: A60764; MUID:90007613; PMID:2571587

A;Accession: A60764

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-377 <HUC>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 9.6e-82;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

```

Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
      |  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy     62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    211 GVEVHNAKTKPREEQYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

Qy    122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPVLD 330

Qy    182 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 228
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    331 DGSFFLYSRLTVDKSRWQEGNVSCSVMHEALHNRFQKSLSLSPGK 377

```

RESULT 7

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;

PID:g6066056

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.
 A;Reference number: A92809; MUID:81007873; PMID:6774012
 A;Contents: myeloma protein Til
 A;Accession: A92809
 A;Molecule type: protein
 A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A;Note: Trp-156 is at or near the complement-binding site
 R;Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A;Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.
 A;Reference number: A90752; MUID:80001357; PMID:113060
 A;Contents: myeloma protein Zie
 A;Accession: A90752
 A;Molecule type: protein
 A;Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-234, 'Z', 236-263, 'BGEPPZ', 269-325 <CON>
 A;Note: this sequence has since been revised
 R;Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.
 A;Reference number: A93132; MUID:80114419; PMID:118920
 A;Contents: Zie
 A;Accession: A93132
 A;Molecule type: protein
 A;Residues: 238-275 <HOF>
 R;Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A;Reference number: A94591
 A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidation states of residues 58, 194, and 197; the amidation states of residues 172-174, 176, and 235 were not determined
 R;Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
 A;Reference number: A90253; MUID:72033500; PMID:4940472
 A;Contents: annotation; myeloma protein Sa, disulfide bonds
 R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A;Title: Structural studies of immunoglobulin G.
 A;Reference number: A93157; MUID:69064124; PMID:5782707
 A;Contents: annotation; Sa, disulfide bonds
 C;Genetics:
 A;Gene: GDB:IGHG2
 A;Cross-references: GDB:119338; OMIM:147110
 A;Map position: 14q32.33-14q32.33
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>
 F;133-202/Domain: immunoglobulin homology <IM2>
 F;239-306/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83,140-200,246-304/Disulfide bonds: #status experimental
 F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.3%; Score 1142.5; DB 1; Length 326;
 Best Local Similarity 94.1%; Pred. No. 1e-81;
 Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

```

Qy      7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
      ||||| : |||||
Db     106 CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 164

Qy     67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
      ||||| : || : ||||| : |||||
Db    165 NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE 224

Qy    127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFF 186
      ||||| : || : ||||| : |||||
Db    225 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGGSFF 284

Qy    187 LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      |||||
Db    285 LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326
  
```

RESULT 8

G4HU

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C;Accession: A90933; A90249; A02150

R;Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933

A;Molecule type: DNA

A;Residues: 1-327 <ELL>

A;Note: the sequence was determined from the germline gene

R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of A gamma4 chain.

A;Reference number: A90249; MUID:70207560; PMID:4192699

A;Accession: A90249

A;Molecule type: protein

A;Residues: 1-30;81-326 <PIN>

C;Genetics:

A;Gene: GDB:IGHG4

A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14q32.33-14q32.33

A;Introns: 99/1; 111/1; 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>

F;240-307/Domain: immunoglobulin homology <IM3>

F;14/Disulfide bonds: interchain (to light chain) #status experimental

F;27-83,141-201,247-305/Disulfide bonds: #status predicted

F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.7%; Score 1135; DB 1; Length 327;

Best Local Similarity 93.7%; Pred. No. 4e-81;

Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

```
Qy      7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     106 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165

Qy     67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     166 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSI EKTISKAKGQPRE 225

Qy     127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 285

Qy     187 LYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK 228
      |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     286 LYSRLTVDKSRWQEGNV FSCSV MHEALHNHYTQKSLSLSPGK 327
```

RESULT 9

G3HUWI

Ig gamma-3 heavy chain disease proteins - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999

C;Accession: A90442; A92219; A90198; A93915; A02149

R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein Wis.

A;Reference number: A90442; MUID:81021548; PMID:6774747

A;Contents: heavy chain disease protein Wis

A;Accession: A90442

A;Molecule type: protein

A;Residues: 1-289 <FRA>

A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain disulfide bond at position 7 in addition to the 11 normally present in the hinge region

A;Note: this protein lacks most of the V region and all of the CH1 region.

Residue 12 corresponds to the beginning of the hinge region of normal gamma-3 chains

A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of
protein Wis
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in
other gamma chains and contains three identical 15-residue segments (29-43, 44-
58, and 59-73) preceded by a similar 17-residue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72
form inter-heavy chain bonds
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure
of the Fc fragment of immunoglobulin G3.
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to
residues 59-289 of protein Wis
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part
of the hinge compared with normal gamma-3 heavy chains
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.;
Hood, L.; Buxbaum, J.N.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene
deletion model.
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-
154, 'D', 156-157, 'N', 159-181, 'A', 183-186; 199-226, 'N', 228-278, 'Y', 280-289 <ALE>
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain
subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.5%; Score 1121; DB 1; Length 289;
Best Local Similarity 90.3%; Pred. No. 4.2e-80;
Matches 204; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

```

Qy      2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
      |  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 123

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      124 GVQVHNAKTKPREQQFNSTFRVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183

Qy      122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243

Qy      182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG 227
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMEALHNRFQKSLSLSPG 289

```

RESULT 10

GHRB

Ig gamma chain C region - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999

C;Accession: A91749; A90290; A93928; A90245; A94416; A02161

R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype.

A;Reference number: A91749; MUID:84030930; PMID:6313520

A;Accession: A91749

A;Molecule type: mRNA

A;Residues: 1-323 <BER>

A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R;Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.

A;Reference number: A90290; MUID:76135469; PMID:1243651

A;Accession: A90290

A;Molecule type: protein

A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>

R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain and identification of two genomic C-gamma genes.

A;Reference number: A93928; MUID:83299917; PMID:6193512

A;Accession: A93928

A;Molecule type: mRNA

A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>

A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112

A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala

R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.

A;Reference number: A90245; MUID:70110015; PMID:5461106

A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and
Wiksell, Stockholm, 1967
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-
232,'Q',234-245,'D',247-255,'G',257-259,'D',261-265,'D',267-279,'W',281-
283,'S',285-322 <HIL>
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical
light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma,
or mu) chains usually stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.2%; Score 918.5; DB 1; Length 323;
Best Local Similarity 71.7%; Pred. No. 2.9e-64;
Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

```

Qy      1 MDKT---HTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
          :|||      ||  | || ||||| |||||:||||| ||||| ||||| ||||| :|||:
Db      91 VDKTVAPSTCSKPTCPPELLGGPSVFIFFPKPKDTLMISRTPEVTCVVVDVSQDDPEVQ 150

Qy      56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
          | ||:: :|  |:  ||:| ||| ||| | : |||| |||: ||| ||||| |||||
Db     151 FTWYINNEQVRTARPPLEQQFNSTIRVVSSTLPITHQDWLRGKEFKCKVHNKALPAPIEK 210

Qy     116 TISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 175
          |||||: ||| ||: |||: | |: |||  |||||: |||||: ||||| ||: |: |||||
Db     211 TISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT 270

Qy     176 PPVLDSGDGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
          | ||||| ||: |||: ||| | ||: ||: ||| ||||| ||||| ||||| |||||
Db     271 PAVLDSGDGFFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK 323

```

RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA
sequences of a single animal.
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 906.5; DB 2; Length 328;
Best Local Similarity 73.2%; Pred. No. 2.6e-63;
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

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Qy      7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
      || ||| |  ||||:|||||||:|||||||:|||||||:|:|:|:|:|
Db     106 CPICPACE-SPGPSVFIFPPKPKDTLMISRTQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy     67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     165 TAQTRPKEEQFNSTYRVVSVLPIQHQQDWLNGKEFKCKVNNKDLPAITRIISKAKQTRE 224

Qy     127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTPPVLDSDGS 184
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     225 PQVYTLPPHAEELSRKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy     185 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
```

RESULT 12

I47159

Ig gamma 2a chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: I47159

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47159

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124

C;Genetics:

A;Gene: IgG2a

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 906.5; DB 2; Length 328;
Best Local Similarity 73.2%; Pred. No. 2.6e-63;
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

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Qy      7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
      || ||| |  ||||:|||||||:|||||||:|||||||:|:|:|:|:|
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Db	106	CPICPACE-SPGPSVFIFPPKPKDTLMISRT PQVTCVVVDVSQENPEVQFSWYVDGVEVH	164
Qy	67	NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE :: : : : : :	126
Db	165	TAQTRPKEEQFNSTYRVVSVLP IQHDWLNGKEFKCKVNNDLPAPITRIISKAKGTRE	224
Qy	127	PQVYTLPSPSRDELTKNQVSLTCLVKGFYPSPDIAVEWESNGQ--PENNYKTPPVLDSDGS : ::: : : : :	184
Db	225	PQVYTLPHPAAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTPPQQDV DGT	284
Qy	185	FFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	228
Db	285	YFLYSKF SVDKASWOGGGI FOCAMHEALHNHYTOKSI SKTPGK	328

I47162

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: I47162

J. Immunol. 153, 3565-3573, 1994

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-277 <KAC>

C; Genetics:

C; Superfamily: immunoglobulin C region; immunoglobulin homology

F;82-151/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 14

G2GP

Ig gamma-2 chain C region - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151

R;Trischmann, T.M.

submitted to the Atlas, April 1975

A;Reference number: A94553

A;Accession: A94553

A;Molecule type: protein

A;Residues: 1-3 <TRI>

R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.

Biochemistry 10, 18-25, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).
III. Amino acid sequence of the region around the half-cystine joining heavy and
light chains.

A;Reference number: A90352; MUID:71058471; PMID:5538606

A;Accession: A90352

A;Molecule type: protein

A;Residues: 4-68 <BIR>

R;Turner, K.J.; Cebra, J.J.

Biochemistry 10, 9-17, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).
II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen
bromide fragments.

A;Reference number: A90359; MUID:71058486; PMID:5538616

A;Accession: A90359

A;Molecule type: protein

A;Residues: 69-133;312-329 <TUR>

R;Tracey, D.E.; Cebra, J.J.

Biochemistry 13, 4796-4803, 1974

A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2
antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665

A;Accession: A90384

A;Molecule type: protein

A;Residues: 134-226 <TRA>

R;Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2
antibodies.

A;Reference number: A90385; MUID:75036073; PMID:4609467

A;Accession: A90385

A;Molecule type: protein

A;Residues: 227-311 <TR2>

R;Oliveira, B.; Lamm, M.E.

Biochemistry 10, 26-31, 1971

A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Reference number: A90354; MUID:71058474; PMID:4922544

A;Contents: annotation; disulfide bonds

A;Note: Cys-16 is involved in a heavy-light chain bond

A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds

C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea
pigs.

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical
light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma,

or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;21-81/Domain: immunoglobulin homology <IM1>

F;135-204/Domain: immunoglobulin homology <IM2>

F;241-310/Domain: immunoglobulin homology <IM3>

F;28-79/Disulfide bonds: #status experimental

F;142-202/Disulfide bonds: #status experimental

F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;248-308/Disulfide bonds: #status experimental

Query Match 71.8%; Score 889; DB 1; Length 329;

Best Local Similarity 72.3%; Pred. No. 6e-62;

Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

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Db     106 TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPTVTCVVVDVSDPEVQFTWFVDNKPV 165

Qy     66  HNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
      |:|:| |||:|:| ||| : |||| | |:| || | ||||| ||| ||
Db     166 GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTGAPR 225

Qy     126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDG 183
      | |||||:|:|:|:|:| |:|:| ||| || | | |||: |:|
Db     226 MPDVYTLPPSRDELSKSKSVTCLIIINFFPADIHVEWASNRVPVSEKEYKNTPIEDADG 285

Qy     184 SFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG 227
      |:| ||||| || | || |:| ||||| |||:| |||
Db     286 SYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
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RESULT 15

I47158

Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: I47158

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47158

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122

C;Genetics:

A;Gene: IgG1

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 885.5; DB 2; Length 328;

Best Local Similarity 72.4%; Pred. No. 1.1e-61;

Matches 163; Conservative 27; Mismatches 32; Indels 3; Gaps 2;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 16, 2004, 09:38:52 ; Search time 34 Seconds
(without alignments)
1371.227 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	ID	Description
No.		%			

1	1238	100.0	228	9	US-09-847-712-2	Sequence 2, Appli
2	1238	100.0	228	10	US-09-840-277-2	Sequence 2, Appli
3	1238	100.0	228	11	US-09-847-249A-2	Sequence 2, Appli
4	1238	100.0	228	11	US-09-843-221A-2	Sequence 2, Appli
5	1238	100.0	228	11	US-09-840-669B-2	Sequence 2, Appli
6	1238	100.0	228	12	US-10-269-806-32	Sequence 32, Appl
7	1238	100.0	228	12	US-10-145-206-2	Sequence 2, Appli
8	1238	100.0	243	12	US-10-269-806-152	Sequence 152, App
9	1238	100.0	250	12	US-10-269-695-243	Sequence 243, App
10	1238	100.0	250	12	US-10-410-998-243	Sequence 243, App
11	1238	100.0	282	10	US-09-840-277-109	Sequence 109, App
12	1238	100.0	401	12	US-09-389-782-8	Sequence 8, Appli
13	1234	99.7	229	14	US-10-215-297-2	Sequence 2, Appli
14	1234	99.7	229	15	US-10-215-298-2	Sequence 2, Appli
15	1234	99.7	248	12	US-10-145-206-111	Sequence 111, App
16	1234	99.7	248	12	US-10-145-206-112	Sequence 112, App
17	1234	99.7	248	12	US-10-145-206-113	Sequence 113, App
18	1234	99.7	252	12	US-10-145-206-114	Sequence 114, App
19	1234	99.7	252	12	US-10-145-206-115	Sequence 115, App
20	1234	99.7	252	12	US-10-145-206-116	Sequence 116, App
21	1234	99.7	252	12	US-10-145-206-117	Sequence 117, App
22	1234	99.7	252	12	US-10-145-206-118	Sequence 118, App
23	1234	99.7	252	12	US-10-145-206-119	Sequence 119, App
24	1234	99.7	252	12	US-10-145-206-120	Sequence 120, App
25	1234	99.7	252	12	US-10-145-206-121	Sequence 121, App
26	1234	99.7	252	12	US-10-145-206-122	Sequence 122, App
27	1234	99.7	261	12	US-10-435-608-6	Sequence 6, Appli
28	1234	99.7	266	12	US-10-390-566-8	Sequence 8, Appli
29	1234	99.7	266	12	US-10-390-566-15	Sequence 15, Appl
30	1234	99.7	266	12	US-10-390-566-21	Sequence 21, Appl
31	1234	99.7	266	12	US-10-390-566-28	Sequence 28, Appl
32	1234	99.7	293	12	US-10-145-206-123	Sequence 123, App
33	1234	99.7	293	12	US-10-145-206-124	Sequence 124, App
34	1234	99.7	302	15	US-10-115-192-12	Sequence 12, Appl
35	1234	99.7	347	9	US-09-796-033-8	Sequence 8, Appli
36	1234	99.7	347	9	US-09-730-465-8	Sequence 8, Appli
37	1234	99.7	347	12	US-10-329-599-8	Sequence 8, Appli
38	1234	99.7	347	14	US-10-091-236-17	Sequence 17, Appl
39	1234	99.7	347	15	US-10-091-313-7	Sequence 7, Appli
40	1234	99.7	347	15	US-10-091-268-7	Sequence 7, Appli
41	1234	99.7	360	12	US-10-390-566-7	Sequence 7, Appli
42	1234	99.7	360	12	US-10-390-566-14	Sequence 14, Appl
43	1234	99.7	360	12	US-10-390-566-20	Sequence 20, Appl
44	1234	99.7	360	12	US-10-390-566-27	Sequence 27, Appl
45	1234	99.7	367	12	US-10-390-566-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
 US-09-847-712-2
 ; Sequence 2, Application US/09847712
 ; Patent No. US20020090646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, CHUAN-FA

```
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-712-2
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Query Match          100.0%; Score 1238; DB 9; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
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RESULT 2

US-09-840-277-2

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; Sequence 2, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHICO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-277-2

Query Match 100.0%; Score 1238; DB 10; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        |||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
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Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
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Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
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RESULT 3

US-09-847-249A-2

; Sequence 2, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-249A-2

Query Match 100.0%; Score 1238; DB 11; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
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Db          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
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Db          121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Qy          181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
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Db          181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

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RESULT 4

US-09-843-221A-2

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; Sequence 2, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-2

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Query Match          100.0%; Score 1238; DB 11; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
          |||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Qy          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
          |||
Db          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Qy          121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
          |||
Db          121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Qy          181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
          |||

```



```
;  NUMBER OF SEQ ID NOS: 199
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 32
;    LENGTH: 228
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthesized Peptide Sequence
US-10-269-806-32
```

RESULT 7

Query Match 100.0%; Score 1238; DB 12; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

```

Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

```

RESULT 8

US-10-269-806-152

; Sequence 152, Application US/10269806

; Publication No. US20030176352A1

; GENERAL INFORMATION:

; APPLICANT: Min, Hosung

; APPLICANT: Sitney, Karen

; APPLICANT: Hartley, Cynthia

; TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic Activity

; FILE REFERENCE: A-750

; CURRENT APPLICATION NUMBER: US/10/269,806

; CURRENT FILING DATE: 2002-10-10

; NUMBER OF SEQ ID NOS: 199

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 152

; LENGTH: 243

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthesized Peptide Sequence

US-10-269-806-152

```

Query Match          100.0%;  Score 1238;  DB 12;  Length 243;
Best Local Similarity 100.0%;  Pred. No. 2e-99;
Matches 228;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

```

|||||
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 9

US-10-269-695-243

; Sequence 243, Application US/10269695
; Publication No. US20030229023A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN DANIEL
; APPLICANT: MIN, HOSUNG
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801A
; CURRENT APPLICATION NUMBER: US/10/269,695
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding peptide capable of binding to Ang-2
US-10-269-695-243

Query Match 100.0%; Score 1238; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.1e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
|||
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
|||
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
|||
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
|||
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 10

US-10-410-998-243

; Sequence 243, Application US/10410998
; Publication No. US20030236193A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN DANIEL
; APPLICANT: MIN, HOSUNG

```
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801A
; CURRENT APPLICATION NUMBER: US/10/410,998
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/10/269,695
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding peptide capable of binding to Ang-2
US-10-410-998-243
```

```
Query Match          100.0%; Score 1238; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.1e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 11

US-09-840-277-109

```
; Sequence 109, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
```

```

; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Echistatin Fc-peptide
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: NdeI site
; NAME/KEY: misc_feature
; LOCATION: (854)..(854)
; OTHER INFORMATION: BamHI site
US-09-840-277-109

```

```

Query Match          100.0%; Score 1238; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 228

```

RESULT 12

```

US-09-389-782-8
; Sequence 8, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-8

```

Query Match 100.0%; Score 1238; DB 12; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.8e-99;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 13

US-10-215-297-2

; Sequence 2, Application US/10215297
; Publication No. US20020192222A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Simister, Neil E.
; APPLICANT: Lencer, Wayne I.
; TITLE OF INVENTION: RECEPTOR SPECIFIC TRANSEPITHELIAL TRANSPORT OF
; TITLE OF INVENTION: THERAPEUTICS
; FILE REFERENCE: S1383/7003
; CURRENT APPLICATION NUMBER: US/10/215,297
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US 08/578,171
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: US 08/374,159
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 09/122,144
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-297-2

Query Match 99.7%; Score 1234; DB 14; Length 229;
Best Local Similarity 99.6%; Pred. No. 4.2e-99;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
        : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 61

Qy     61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
```

```

Db          62 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 121
Qy          121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db          122 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Qy          181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
Db          182 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 229

```

RESULT 14

US-10-215-298-2

```

; Sequence 2, Application US/10215298
; Publication No. US20030012789A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Simister, Neil E.
; APPLICANT: Lencer, Wayne I.
; TITLE OF INVENTION: RECEPTOR SPECIFIC TRANSEPITHELIAL TRANSPORT OF
THERAPEUTICS
; FILE REFERENCE: S1383/7003
; CURRENT APPLICATION NUMBER: US/10/215,298
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US 09/122,144
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-298-2

```

```

Query Match          99.7%; Score 1234; DB 15; Length 229;
Best Local Similarity 99.6%; Pred. No. 4.2e-99;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
: |||||
Db          2 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 61
Qy          61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db          62 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 121
Qy          121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db          122 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Qy          181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
Db          182 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 229

```

RESULT 15

US-10-145-206-111

```

; Sequence 111, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TALL-1 inhibitory peptibodies
US-10-145-206-111

```

```

Query Match          99.7%; Score 1234; DB 12; Length 248;
Best Local Similarity 99.6%; Pred. No. 4.6e-99;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
        : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 80

Qy      61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 140

Qy     121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 200

Qy     181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 248

```

```

Search completed: January 16, 2004, 09:46:30
Job time : 34 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 16, 2004, 09:36:27 ; Search time 36 Seconds
(without alignments)
1634.333 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	ID			Description

1	1233	99.6	471	4	Q8TC77	Q8tc77	homo sapien
2	1233	99.6	701	4	Q96PQ8	Q96pq8	homo sapien
3	1142	92.2	521	4	Q8N4Y9	Q8n4y9	homo sapien
4	1135	91.7	473	4	Q8TC63	Q8tc63	homo sapien
5	1131	91.4	509	4	Q8NF17	Q8nf17	homo sapien
6	909	73.4	337	6	Q95M34	Q95m34	equus cabal
7	831.5	67.2	469	11	Q8R3V9	Q8r3v9	mus musculu
8	828.5	66.9	463	11	Q99LC4	Q99lc4	mus musculu
9	824.5	66.6	437	11	Q9R1A4	Q9r1a4	mus musculu
10	811	65.5	473	11	Q9D8L4	Q9d8l4	mus musculu
11	805	65.0	468	11	Q99L31	Q99l31	mus musculu
12	805	65.0	473	11	Q99L25	Q99l25	mus musculu
13	780	63.0	473	11	Q91Z05	Q91z05	mus musculu
14	780	63.0	474	11	Q8R3H6	Q8r3h6	mus musculu
15	358	28.9	375	4	Q9BSZ1	Q9bsz1	homo sapien
16	358	28.9	597	4	Q9BU10	Q9bu10	homo sapien
17	358	28.9	597	4	Q9BQB8	Q9bqb8	homo sapien
18	358	28.9	597	4	Q96BB9	Q96bb9	homo sapien
19	348	28.1	588	4	Q8WUX4	Q8wux4	homo sapien
20	348	28.1	613	4	Q96EY0	Q96ey0	homo sapien
21	348	28.1	613	4	Q8WUK1	Q8wuk1	homo sapien
22	348	28.1	614	4	Q96GA6	Q96ga6	homo sapien
23	348	28.1	618	4	Q96AA6	Q96aa6	homo sapien
24	347	28.0	613	11	Q8VCX7	Q8vcx7	mus musculu
25	272.5	22.0	684	13	Q90544	Q90544	ginglymosto
26	272	22.0	384	4	Q9UP60	Q9up60	homo sapien
27	272	22.0	493	4	Q8NCL6	Q8ncl6	homo sapien
28	272	22.0	494	4	Q96K68	Q96k68	homo sapien
29	272	22.0	496	4	Q96KX8	Q96kx8	homo sapien
30	269	21.7	496	4	Q96DK0	Q96dk0	homo sapien
31	269	21.7	499	4	Q8N5K4	Q8n5k4	homo sapien
32	267	21.6	416	4	Q9NPP6	Q9npp6	homo sapien
33	267	21.6	497	4	Q8WY24	Q8wy24	homo sapien
34	267	21.6	500	4	Q9BRV0	Q9brv0	homo sapien
35	261	21.1	486	11	Q91Z07	Q91z07	mus musculu
36	261	21.1	487	11	Q99KA4	Q99ka4	mus musculu
37	260	21.0	426	11	Q9DCD9	Q9dcd9	mus musculu
38	253.5	20.5	481	11	Q91WT3	Q91wt3	mus musculu
39	253.5	20.5	481	11	Q91WT1	Q91wt1	mus musculu
40	253.5	20.5	482	11	Q91X92	Q91x92	mus musculu
41	253.5	20.5	482	11	Q8K172	Q8k172	mus musculu
42	253.5	20.5	484	11	Q8VEA0	Q8vea0	mus musculu
43	253.5	20.5	488	11	Q91WR1	Q91wr1	mus musculu
44	253.5	20.5	488	11	Q8K0F2	Q8k0f2	mus musculu
45	253.5	20.5	489	11	Q8VCX4	Q8vcx4	mus musculu

ALIGNMENTS

RESULT 1

Q8TC77

ID	Q8TC77	PRELIMINARY;	PRT;	471 AA.
AC	Q8TC77;			
DT	01-JUN-2002	(TrEMBLrel. 21, Created)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)		
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)		

DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC024289; AAH24289.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 99.6%; Score 1233; DB 4; Length 471;
 Best Local Similarity 100.0%; Pred. No. 3.9e-108;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD	61
Db	245	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD	304
Qy	62	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121
Db	305	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	364
Qy	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	181
Db	365	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	424
Qy	182	DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK	228
Db	425	DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK	471

RESULT 2

Q96PQ8

ID Q96PQ8 PRELIMINARY; PRT; 701 AA.
 AC Q96PQ8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Factor VII active site mutant immunoconjugate.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.;
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
 RT cells for immunotherapy in mouse models of prostatic cancer."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AF272774; AAK58686.1; -.
 DR HSSP; P00761; 1AN1.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00047; ig; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFBLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 99.6%; Score 1233; DB 4; Length 701;
 Best Local Similarity 100.0%; Pred. No. 6.4e-108;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	61
Db	475	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	534
Qy	62	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121
Db	535	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	594
Qy	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	181

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Db          595 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS 654
Qy          182 DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 228
          |||
Db          655 DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 701

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RESULT 3

Q8N4Y9

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ID   Q8N4Y9          PRELIMINARY;          PRT;          521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells from Tonsils;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

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Query Match          92.2%; Score 1142; DB 4; Length 521;
Best Local Similarity 92.1%; Pred. No. 1.8e-99;
Matches 209; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

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Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD 61
          |  |||
Db          295 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVQFKWYVD 354

Qy          62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
          |||
Db          355 GVEVHNAKTKPREEQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 414

Qy          122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS 181
          |||
Db          415 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 474

Qy          182 DGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 228
          |||
Db          475 DGSFFLYSKLTVDKSRWQQGNIFCFSVMHEALHNRFTQKSLSLSPGK 521

```

RESULT 4

Q8TC63

ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 91.7%; Score 1135; DB 4; Length 473;
Best Local Similarity 93.7%; Pred. No. 7.1e-99;
Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
|| ||||| ||||||||||||||||||||||||||||||||| |||||:|||||||
Db 252 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 311
Qy 67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
|||||||:||||||||||||||||||||||||||||||| ||: |||||||||
Db 312 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE 371
Qy 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 186
|||||||:|:|:||||||||||||||||||||||||||||||| |||||||||
Db 372 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 431
Qy 187 LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
|||:|||||||:||||||||||||||||||||||||||| ||
Db 432 LYSRLTVDKSRWQEGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 5

Q8NF17

ID Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE FLJ00385 protein (Fragment).
 GN FLJ00385.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
 RT "The nucleotide sequence of a long cDNA clone isolated from human
 RT spleen.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK090464; BAC03445.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match 91.4%; Score 1131; DB 4; Length 509;
 Best Local Similarity 92.0%; Pred. No. 1.9e-98;
 Matches 207; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
 | |||||
 Db 214 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 273
 QY 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
 |||||:|:|
 Db 274 GVEVHNAKTKPREEQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 333
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
 |||||:|:|
 Db 334 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 393
 QY 182 DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSP 226
 |||||:|:|
 Db 394 DGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRFQKSLSLSP 438

RESULT 6

Q95M34

ID Q95M34 PRELIMINARY; PRT; 337 AA.
 AC Q95M34;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).
 GN IGHC1.
 OS Equus caballus (Horse).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC024405; AAH24405.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 67.2%; Score 831.5; DB 11; Length 469;
 Best Local Similarity 63.8%; Pred. No. 3.5e-70;
 Matches 143; Conservative 41; Mismatches 35; Indels 5; Gaps 2;

Qy 7 CPP--CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 64
 | | | | : | | : | | | | | | | | : | | : | | | | | : | | : | | | | |
 Db 249 CKPCICTVPEV---SSVFIFPPKPKDVLTIITLTPKVTCVVDISKDDPEVQFSWFVDDVE 305

 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 | | : | | | | | : | | : | | | | | | | : | | : | | : | | : | | : | | : | |
 Db 306 VHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 365

 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 184
 : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
 Db 366 KAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 425

 Qy 185 FFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 228
 : | : | | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
 Db 426 YFVYSKLVNQSKNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK 469

RESULT 8

Q99LC4

ID Q99LC4 PRELIMINARY; PRT; 463 AA.
 AC Q99LC4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1810060O09 gene.
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC003435; AAH03435.1; -.
 DR HSSP; P01842; 7FAB.

DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 66.9%; Score 828.5; DB 11; Length 463;
 Best Local Similarity 63.4%; Pred. No. 6.6e-70;
 Matches 142; Conservative 42; Mismatches 35; Indels 5; Gaps 2;

Qy 7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 | | | | : | | : | | | | | | | | : | | : | | | | | : | : | | | : | : | | |
 Db 243 CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTCTVVVDISKDDPEVQFSWFVDDVE 299
 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 | | | : | : | | | | : | | : | | | | | | | : | : | : | | | | | | | : |
 Db 300 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 359
 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS 184
 : | | | | : | | : : : | : | | | | : : | : | | | | | | | | | | : : | : | |
 Db 360 KAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVQWNGQPAENYKNTQPIMDTDGS 419
 Qy 185 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
 : | : | | | | | | | : | | | : | | : | | : | | | | : | : | | | | | | |
 Db 420 YFIYSKLVQKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK 463

RESULT 9

Q9R1A4

ID Q9R1A4 PRELIMINARY; PRT; 437 AA.
 AC Q9R1A4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Gamma1 heavy chain of Mab7 (Fragment).
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFV).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF152372; AAD40243.1; -.
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1 1
 FT NON_TER 437 437
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 66.6%; Score 824.5; DB 11; Length 437;
 Best Local Similarity 62.9%; Pred. No. 1.5e-69;
 Matches 141; Conservative 43; Mismatches 35; Indels 5; Gaps 2;

Qy 7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 | | | | | : | | | | | | | | | | : | | | | | | | | : | | | | | | | |
 Db 217 CKPCICTVPEV---SSVFIFPPKPKDVLTLITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 273
 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 | | | : | | | | | : | | | | | | | | : | | | | | | | | : | | | | | | | |
 Db 274 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 333
 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS 184
 : | | | | : | | : : : | : | | | | : : | : | | | | : | | | | | : | : | | |
 Db 334 KAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 393
 Qy 185 FFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 228
 : | : | | | | | | | : | | | : | | | | | : | : | | | | | | | | | |
 Db 394 YFVYSKLVQKSNWEAGNTFTCSVLHEGLHNHTEKNLSHSPGK 437

RESULT 10
 Q9D8L4

ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
 AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 181006009Rik protein.
 GN IGH-1 OR 181006009RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK007918; BAB25349.1; -.
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 65.5%; Score 811; DB 11; Length 473;
 Best Local Similarity 64.0%; Pred. No. 3.1e-68;
 Matches 142; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

Qy 7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
 ||||| |:|||||||:||||| || ||||| :| ||||||||| :||:|: |:|:|: |||||
 Db 252 CPPCAAPDLLGGPSVFIFPPKIKDVLMI SLSPMVT CVVVDVSEDDPDVQISW FVN NVEVH 311

 Qy 67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
 |:|: | ||||| ||||| | : |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 312 TAQTQTHREDYNSTLRVVSALPIQH QDWM SGEKFKCKVNNRALPSPIEKTISKPRGPVRA 371

 Qy 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 186
 ||||| ||| :|:|:| : |||||:| |||:|:|:| |||:| ||| | |||||:|
 Db 372 PQVYVLP PPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYF 431

 Qy 187 LYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK 228
 :||| | || |:|:|:|:|:|:| |||| | |:| | ||
 Db 432 MYSLRVQKSTWERSL FACS VVHEGLHNHLTTKTISRSLGK 473

RESULT 11

Q99L31

ID Q99L31 PRELIMINARY; PRT; 468 AA.
 AC Q99L31;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1810060009 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC003878; AAH03878.1; -.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 65.0%; Score 805; DB 11; Length 468;
 Best Local Similarity 65.2%; Pred. No. 1.1e-67;
 Matches 146; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 7 CPP--CPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 ||| |||| |||||:|||| || |||| :| ||||| ||| :||:| :||:| ||
 Db 245 CPPCKCPAPNLLGGPSVFI FPPKIKDVLMSLSPMVTCTVVVDVSEDDPDVQISWFVNNE 304
 QY 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 | :|:| | |||| |||| | : ||||:| |||: ||||| |||: |||| ||
 Db 305 VLTAQTQTHREDYNSTLRVVSALPIQHQDWMMSGKEFKCKVNNKALPAPIERTISKPKGSV 364
 QY 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 184
 | |||| ||| :||:| ||: |||:| | | | ||| :||: | ||| | ||||| ||
 Db 365 RAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDSDGS 424
 QY 185 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
 :||: |||| | :| | : ||||: || ||||: || | | :|||
 Db 425 YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 468

RESULT 12

Q99L25

ID Q99L25 PRELIMINARY; PRT; 473 AA.
 AC Q99L25;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 181006009 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC003888; AAH03888.1; -.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 65.0%; Score 805; DB 11; Length 473;
Best Local Similarity 65.2%; Pred. No. 1.1e-67;
Matches 146; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

```
Qy      7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
      ||| ||| ||||| |||||:|||| || ||| :| ||||| ||| :||:| :||:| ||
Db      250 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMI SLSPMVTCVVVDVSEDDPDVQISWFVNNVE 309

Qy      65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
      | |:|: | ||| ||| | : |||:| |||:| ||||| |||:| ||| ||
Db      310 VLTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKALPAPIERTISKPKGSV 369

Qy      125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
      | ||| ||| :||| ||:| ||:| | | | ||| :||: | ||| | ||||| ||
Db      370 RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDSGDS 429

Qy      185 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      :|:|||| |:| | : | :|||:| | |||:| || | :|||
Db      430 YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 473
```

RESULT 13

Q91Z05

ID Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.0%; Score 780; DB 11; Length 473;
Best Local Similarity 61.8%; Pred. No. 2.6e-65;

Matches 141; Conservative 34; Mismatches 47; Indels 6; Gaps 1;

```
Qy      7 CPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
      |||      |||| | |||||:| || |||| | |:||||||| :| |:| :|:|
Db      246 CPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWV 305

Qy      61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
      : |||| | |:| | |||| |||| | : ||||:| |:| |:| |:| |:|
Db      306 NNVEVHTAQTQTHREDYNSTIRVVSALPIQHQQDWMMSGKEFKCKVNNKDLPSPIERTISKI 365

Qy      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
      || | |||| ||| :|:|: ||||| || | ||:| || | ||| | |||
Db      366 KGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFGNPGDISVEWTSNGHTEENYKDTAPVLD 425

Qy      181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      ||| |:| ||| : | |:| : |||:| || | |:| |:| :|:| |||
Db      426 SDGSYFIYSKLDIKTSKWEKTDSCNVRHEGLKNYYLKKTISRSPGK 473
```

RESULT 14

Q8R3H6

ID Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 63.0%; Score 780; DB 11; Length 474;

Best Local Similarity 61.8%; Pred. No. 2.6e-65;

Matches 141; Conservative 34; Mismatches 47; Indels 6; Gaps 1;

```
Qy      7 CPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
      |||      |||| | |||||:| || |||| | |:||||||| :| |:| :|:|
Db      247 CPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWV 306

Qy      61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
```

```

      : |||| |:: | |||| |||| | : ||||::|||:||||:| |::|||:||||
Db      307 NNVEVHTAQQTQTHREDYNSTIRVVSALPIQHQDWMMSGKEFKCKVNNKDLPSPIERTISKI 366

Qy      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
      || | |||| || |::: ||||| || | ||: || | || | || | ||||
Db      367 KGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLD 426

Qy      181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      ||||:|:|||| : |::: : |||:| || | |:| :|::| ||||
Db      427 SDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474

```

RESULT 15

Q9BSZ1

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ID   Q9BSZ1          PRELIMINARY;          PRT;    375 AA.
AC   Q9BSZ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004476; AAH04476.1; -.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE    375 AA;  41314 MW;  B1A0A0998F473619 CRC64;

```

```

Query Match          28.9%;  Score 358;  DB 4;  Length 375;
Best Local Similarity 34.1%;  Pred. No. 1.5e-25;
Matches    73;  Conservative    48;  Mismatches    85;  Indels      8;  Gaps      6;

```

```

Qy      21 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 80
      || || |:: :::: ||::| |:: | | :| | | | |::|
Db      146 VFAIPPS-FASIFLTAKSTKLTCLVTDLTFTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 203

Qy      81 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 139
      : | :: || :|: | |:: ||:|::|||: || | || |||:|::|
Db      204 FSAVGEASICEDDWNSEGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQL 263

Qy      140 T-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTV 194
      : :||| || |::|: || | || | |::: | :| :| |||
Db      264 NLRESATITCLVTGFSPADVVFQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS 323

```


Qy 195 KSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 228
: | | : | | | | | : : : | |
Db 324 EEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 357

Search completed: January 16, 2004, 09:38:45
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 16, 2004, 09:36:26 ; Search time 17 Seconds
(without alignments)
630.711 Million cell updates/sec

Title: US-09-843-221A-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1233	99.6	330	1	GC1_HUMAN	P01857 homo sapien
2	1142.5	92.3	326	1	GC2_HUMAN	P01859 homo sapien
3	1135	91.7	327	1	GC4_HUMAN	P01861 homo sapien
4	1126	91.0	290	1	GC3_HUMAN	P01860 homo sapien
5	918.5	74.2	323	1	GC_RABIT	P01870 oryctolagus
6	889	71.8	329	1	GC2_CAVPO	P01862 cavia porce
7	845.5	68.3	329	1	GC3_MOUSE	P22436 mus musculu
8	838	67.7	333	1	GCB_RAT	P20761 rattus norv
9	834.5	67.4	398	1	GC3M_MOUSE	P03987 mus musculu
10	818.5	66.1	326	1	GC1_RAT	P20759 rattus norv
11	817.5	66.0	324	1	GC1_MOUSE	P01868 mus musculu
12	812.5	65.6	393	1	GC1M_MOUSE	P01869 mus musculu
13	809.5	65.4	329	1	GCC_RAT	P20762 rattus norv
14	809	65.3	330	1	GCAA_MOUSE	P01863 mus musculu
15	804	64.9	399	1	GCAM_MOUSE	P01865 mus musculu
16	802	64.8	335	1	GCAB_MOUSE	P01864 mus musculu
17	785.5	63.4	322	1	GCA_RAT	P20760 rattus norv

18	779	62.9	336	1	GCB_MOUSE	P01866	mus musculu
19	774	62.5	405	1	GCBM_MOUSE	P01867	mus musculu
20	358	28.9	454	1	MUC_HUMAN	P01871	homo sapien
21	357	28.8	455	1	MUC_MOUSE	P01872	mus musculu
22	356	28.8	391	1	MUCB_HUMAN	P04220	homo sapien
23	354	28.6	421	1	EPC_MOUSE	P06336	mus musculu
24	353	28.5	429	1	EPC_RAT	P01855	rattus norv
25	352	28.4	428	1	EPC_HUMAN	P01854	homo sapien
26	347	28.0	476	1	MUCM_MOUSE	P01873	mus musculu
27	342	27.6	458	1	MUC_RABIT	P03988	oryctolagus
28	332	26.8	450	1	MUC_CANFA	P01874	canis famil
29	332	26.8	454	1	MUC_MESAU	P06337	mesocricetu
30	332	26.8	479	1	MUCM_RABIT	P04221	oryctolagus
31	329	26.6	457	1	MUC_SUNMU	P20768	suncus muri
32	297	24.0	438	1	HVC2_HETFR	P23085	heterodontu
33	295.5	23.9	299	1	ALC_RABIT	P01879	oryctolagus
34	287.5	23.2	438	1	HVCS_HETFR	P23087	heterodontu
35	287.5	23.2	446	1	MUC_CHICK	P01875	gallus gall
36	278.5	22.5	461	1	HVCM_HETFR	P23088	heterodontu
37	276.5	22.3	393	1	HVC3_HETFR	P23086	heterodontu
38	272	22.0	353	1	ALC1_HUMAN	P01876	homo sapien
39	272	22.0	370	1	HVC1_HETFR	P23084	heterodontu
40	267.5	21.6	353	1	ALC1_GORGO	P20758	gorilla gor
41	267	21.6	340	1	ALC2_HUMAN	P01877	homo sapien
42	248.5	20.1	481	1	MUCM ICTPU	P23735	ictalurus p
43	245	19.8	344	1	ALC_MOUSE	P01878	mus musculu
44	179	14.5	513	1	SHS1_MOUSE	P97797	m protein-t
45	177.5	14.3	105	1	LAC1_MOUSE	P01843	mus musculu

ALIGNMENTS

RESULT 1

GC1_HUMAN

ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170(1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181(1970).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
 CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
 CC MARKER & THE G1M (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES

CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.

CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.

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DR EMBL; J00228; AAC82527.1; ALT_INIT.

DR PIR; A93433; GHHU.

DR PDB; 1FC1; 15-JUL-92.

DR PDB; 1FC2; 15-JUL-92.

DR PDB; 1AJ7; 12-NOV-97.

DR PDB; 1D5B; 09-FEB-00.

DR PDB; 1D5I; 09-FEB-00.

DR PDB; 1D6V; 04-OCT-00.

DR PDB; 1DN2; 17-MAY-00.

DR PDB; 1E4K; 06-JUN-01.

DR PDB; 1FCC; 20-JUL-95.

DR PDB; 1HZH; 12-JUN-02.

DR PDB; 1I7Z; 08-AUG-01.

DR PDB; 1IIS; 16-MAY-01.

DR PDB; 1IIX; 16-MAY-01.

DR PDB; 1L6X; 10-APR-02.

DR PDB; 2RCS; 12-NOV-97.

DR Genew; HGNC:5525; IGHG1.

DR MIM; 147100; -.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0003823; F:antigen binding activity; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW 3D-structure.

FT NON_TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.

FT DISULFID 27 83

FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .).

FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.

FT	VARIANT	97	97	K -> R (IN G1M(3) MARKER).
FT				/FTId=VAR_003886.
FT	VARIANT	239	239	D -> E (IN G1M(NON-1) MARKER).
FT				/FTId=VAR_003887.
FT	VARIANT	241	241	L -> M (IN G1M(NON-1) MARKER).
FT				/FTId=VAR_003888.
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	147	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	166	
FT	TURN	168	171	
FT	STRAND	176	179	
FT	TURN	180	181	
FT	STRAND	182	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	260	265	
FT	STRAND	270	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	305	312	
FT	TURN	313	314	
FT	TURN	316	317	
FT	STRAND	320	325	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 99.6%; Score 1233; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 2.2e-93;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	61
Db	104	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	163
Qy	62	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121
Db	164	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	223
Qy	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	181
Db	224	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD	283
Qy	182	DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK	228

RESULT 2

GC2_HUMAN

ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).

RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).

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DR EMBL; J00230; AAB59393.1; -.
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; 1FC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.

FT	DOMAIN	220	326	CH3.
FT	DISULFID	14	14	INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID	27	83	
FT	DISULFID	102	102	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	103	103	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	140	200	
FT	DISULFID	246	304	
FT	SITE	156	156	AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT	MOD_RES	326	326	REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT	VARIANT	60	60	S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT				/FTid=VAR_003889.
FT	CONFLICT	109	109	C -> S (IN REF. 3).
SQ	SEQUENCE	326 AA;	35884 MW;	8310878C6878CF9C CRC64;

[illegible]

RESULT 3


```

Db      226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 285
      |||:|||||:|:|||||
Qy      187 LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
      |||:|||||:|:|||||
Db      286 LYSRLTVDKSRWQEGNVFCSCVMHEALHNHYTQKSLSLSLGK 327

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RESULT 4

GC3_HUMAN

```

ID      GC3_HUMAN          STANDARD;          PRT;          290 AA.
AC      P01860;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN      IGHG3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE (DISEASE PROTEIN WIS).
RX      MEDLINE=81021548; PubMed=6774747;
RA      Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT      "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT      gamma 3 heavy-chain disease protein Wis.";
RL      Biochemistry 19:4304-4308(1980).
RN      [2]
RP      REVISIONS TO 12-97 (PROTEIN WIS).
RX      MEDLINE=77118561; PubMed=402363;
RA      Michaelsen T.E., Frangione B., Franklin E.C.;
RT      "Primary structure of the 'hinge' region of human IgG3. Probable
RT      quadruplication of a 15-amino acid residue basic unit.";
RL      J. Biol. Chem. 252:883-889(1977).
RN      [3]
RP      REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX      MEDLINE=77021516; PubMed=823945;
RA      Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT      "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT      Structure of the Fc fragment of immunoglobulin G3.";
RL      Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN      [4]
RP      SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX      MEDLINE=82247835; PubMed=6808505;
RA      Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA      Franklin E.C., Hood L., Buxbaum J.N.;
RT      "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT      gene deletion model.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC      -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC      INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC      NORMALLY PRESENT IN THE HINGE REGION.
CC      -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC      -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC      REF.2.
CC      -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION

```

CC AND ALL OF THE CH1 REGION.
 CC -!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
 CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
 CC GAMMA-3 HEAVY CHAINS.
 CC -!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
 CC OR ANOTHER GAMMA CHAIN SUBCLASS.
 CC -!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
 CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
 CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 CC SEGMENT (12-28).

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DR EMBL; J00231; AAA52805.1; ALT_SEQ.
 DR HSSP; P01857; 1FC1.
 DR Genew; HGNC:5527; IGHG3.
 DR MIM; 147120; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
 KW Pyrrolidone carboxylic acid.
 FT DOMAIN 12 73 HINGE.
 FT DOMAIN 74 183 CH2.
 FT DOMAIN 184 289 CH3.
 FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .).
 FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).
 FT MOD_RES 290 290 REMOVED POST-TRANSLATIONALLY.

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FT    VARIANT      126    127    QV -> EB (IN ZUC).
FT                                     /FTid=VAR_003890.
FT    VARIANT      134    134    P -> L (IN OMM).
FT                                     /FTid=VAR_003891.
FT    VARIANT      139    139    F -> Y (IN OMM).
FT                                     /FTid=VAR_003892.
FT    VARIANT      182    182    T -> A (IN OMM).
FT                                     /FTid=VAR_003893.
FT    VARIANT      227    227    S -> N (IN OMM).
FT                                     /FTid=VAR_003894.
FT    VARIANT      227    227    MISSING (IN ZUC).
FT                                     /FTid=VAR_003895.
FT    VARIANT      279    279    F -> Y (IN OMM).
FT                                     /FTid=VAR_003896.
SQ    SEQUENCE     290 AA;  32331 MW;  E69CBC95705B2F46 CRC64;

```

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Query Match          91.0%; Score 1126; DB 1; Length 290;
Best Local Similarity 90.3%; Pred. No. 9.6e-85;
Matches 205; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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```

Qy      2 DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
      |  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      64 DTPPPCPRCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKWYVD 123

Qy      62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
      ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     124 GVQVHNAKTKPREQQFNSTFRVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183

Qy     122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243

Qy     182 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK 228
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     244 DGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRFQKSLSLSPGK 290

```

RESULT 5

GC_RABIT

```

ID    GC_RABIT          STANDARD;          PRT;    323 AA.
AC    P01870;
DT    21-JUL-1986 (Rel. 01, Created)
DT    21-JUL-1986 (Rel. 01, Last sequence update)
DT    15-SEP-2003 (Rel. 42, Last annotation update)
DE    Ig gamma chain C region.
OS    Oryctolagus cuniculus (Rabbit).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX    NCBI_TaxID=9986;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=84030930; PubMed=6313520;
RA    Bernstein K.E., Alexander C.B., Mage R.G.;
RT    "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT    F-I haplotype.";
RL    Immunogenetics 18:387-397(1983).
RN    [2]

```

RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).

RN [3]

RP SEQUENCE OF 88-266 FROM N.A.

RX MEDLINE=83299917; PubMed=6193512;

RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;

RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).

RN [4]

RP SEQUENCE OF 132-161.

RX MEDLINE=70110015; PubMed=5461106;

RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;

RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";

RL Biochem. J. 116:249-259(1970).

RN [5]

RP SEQUENCE OF 129-131 AND 155-322.

RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;

RL (In) Killander J. (eds.);

RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).

CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

CC

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DR EMBL; M16426; AAA31289.1; -.

DR PIR; A91749; GHRB.

DR HSSP; P01857; 1FC1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Repeat.

FT NON_TER 1 1

FT DOMAIN 6 96 IG-LIKE 1.

FT DOMAIN 114 213 IG-LIKE 2.

FT DOMAIN 222 318 IG-LIKE 3.

FT VARIANT 104 104 T -> M (IN D11 MARKER).

FT VARIANT 185 185 T -> A (IN E15 MARKER).

FT CONFLICT 48 48 N -> E (IN REF. 2).

FT	CONFLICT	71	71	V -> VPV (IN REF. 2).
FT	CONFLICT	144	144	Q -> E (IN REF. 3 AND 4).
FT	CONFLICT	173	173	N -> D (IN REF. 5).
FT	CONFLICT	187	187	Q -> E (IN REF. 3 AND 5).
FT	CONFLICT	201	201	N -> D (IN REF. 5).
FT	CONFLICT	218	218	Q -> E (IN REF. 5).
FT	CONFLICT	233	233	E -> Q (IN REF. 5).
FT	CONFLICT	246	246	N -> D (IN REF. 5).
FT	CONFLICT	256	256	E -> G (IN REF. 5).
FT	CONFLICT	260	260	N -> D (IN REF. 5).
FT	CONFLICT	266	266	N -> D (IN REF. 5).
FT	CONFLICT	280	280	Y -> W (IN REF. 5).
FT	CONFLICT	284	284	N -> S (IN REF. 5).
SQ	SEQUENCE	323 AA;	35404 MW;	69E8AA118D579A8B CRC64;

Query Match 74.2%; Score 918.5; DB 1; Length 323;
 Best Local Similarity 71.7%; Pred. No. 8.9e-68;
 Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

Qy	1	MDKT---HTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK	55
		: : :	
Db	91	VDKTVAPSTCSKPTCPPPELLGGPSVFI FPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQ	150
Qy	56	FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK	115
		:: : : : : :	
Db	151	FTWYINNEQVRTARPLREQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEK	210
Qy	116	TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT	175
		: : : : : : : : :	
Db	211	TISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT	270
Qy	176	PPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK	228
		: : : : : : : :	
Db	271	PAVLDSGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK	323

RESULT 6

GC2_CAVPO

ID GC2_CAVPO STANDARD; PRT; 329 AA.
 AC P01862;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig

RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
 RT half-cystine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4804-4811(1974).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71058474; PubMed=4922544;
 RA Oliveira B., Lamm M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RL Biochemistry 10:26-31(1971).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 CC 13 INBRED GUINEA PIGS.
 DR PIR; A94553; G2GP.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 71.8%; Score 889; DB 1; Length 329;
 Best Local Similarity 72.3%; Pred. No. 2.3e-65;
 Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

Qy 6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
 ||| || || |||||:||||||| || ||||| :|||:| :|| |
 Db 106 TCPKCPPPENLGGPSVFI FPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFDNKPV 165

Qy 66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
 ||:|||| ||||:|:| ||| : |||| |||:|||| ||||| ||||| || ||
 Db 166 GNAETKPRVEQYNTTFRVESVLPIHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR 225

Qy 126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDG 183
 | |||||:|:|:|:|:| :|:| ||| || | | |||:|:|
 Db 226 MPDVYTLPPSRDELSKSKSVTCLIIFFPADIHVEWASNRVPVSEKEYKNTPIEDADG 285

Qy 184 SFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG 227
 |:||||||| || || |:| ||||| ||||:| |||
 Db 286 SYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329

RESULT 7

GC3_MOUSE

ID GC3_MOUSE STANDARD; PRT; 329 AA.

AC P22436;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ig gamma-3 chain C region, secreted form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85027161; PubMed=6092053;

RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;

RT "Structural analysis of the murine IgG3 constant region gene.;"

RL EMBO J. 3:2041-2046(1984).

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DR EMBL; J00451; -; NOT_ANNOTATED_CDS.

DR PIR; B02156; G3MSC.

DR HSSP; P01857; 1FC1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 68.3%; Score 845.5; DB 1; Length 329;
 Best Local Similarity 67.0%; Pred. No. 8.1e-62;
 Matches 150; Conservative 34; Mismatches 37; Indels 3; Gaps 1;

Qy 8 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 || || :|||||:||||| ||| ||:||||| :||:| :||| |
 Db 106 PPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCTVVVDVSEDDPDVHVSFVDNKE 165
 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 || | |:| | ||||:| | | : | | | : | | : | | | | | : | | | | | :
 Db 166 VHTAWTQPREAQYNSTFRVVSALPIQHQQDWMRGKEFKCKVNNKALPAPIERTISKPKGRA 225
 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS 184
 : |||||:| | :::| :||| | | : | | | | | : | | | | | :
 Db 226 QTPQVYTI PPPREQMSKKKVSILTCLVTNFFSEAI SVEWERNGELEQDYKNTPPILDSGT 285
 Qy 185 FFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 228
 : ||||| | | | : | | | : | | | | | : | | | | | |
 Db 286 YFLYSKLTVDTD SWLQGEIFTCSV VHEALHNHHTQKNLSRSPGK 329

RESULT 8

GCB_RAT
 ID GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2B chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 DR PIR; PS0018; PS0018.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 96 IG-LIKE 1.
 FT DOMAIN 124 223 IG-LIKE 2.
 FT DOMAIN 232 328 IG-LIKE 3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 80
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 147 207
 FT DISULFID 253 311
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 67.7%; Score 838; DB 1; Length 333;
 Best Local Similarity 66.4%; Pred. No. 3.3e-61;
 Matches 148; Conservative 33; Mismatches 42; Indels 0; Gaps 0;

Qy 6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
 || || ||||| ||||| : ||||| | : || : ||||| || : || : || : || : ||
 Db 111 TCHKCPVPELLGGPSVFI FPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWVNNVEV 170
 Qy 66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
 | : || : ||||| ||||| : |||| | : |||| : |||| : |||| : ||||| || |
 Db 171 HTAQTPREEQYNSTFRVVSALPIQHQQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVR 230
 Qy 126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 185
 : |||| : | : |||| ||||| || || : || || || || || || || : |||||
 Db 231 KPQVYVMGPPTQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSF 290
 Qy 186 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 | : |||| | : |||| | ||||| || |||| : || : || || ||
 Db 291 FMYSKLNVERSRWDSRAPFVCSVHEGLHNHHVEKSISRPPGK 333

RESULT 9

GC3M_MOUSE

ID GC3M_MOUSE STANDARD; PRT; 398 AA.
 AC P03987;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-3 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene."
 RL EMBO J. 3:2041-2046(1984).
 RN [2]
 RP SEQUENCE OF 328-398 FROM N.A.

RX MEDLINE=84041483; PubMed=6314258;
 RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
 RA Wall R.;
 RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
 RT segment.";
 RL Nucleic Acids Res. 11:6775-6785(1983).
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 DR EMBL; J00451; AAB59655.1; -.
 DR EMBL; V01526; CAA24767.1; ALT_SEQ.
 DR PIR; A02156; G3MSM.
 DR HSSP; P01857; 1FC1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 FT TRANSMEM 346 362 POTENTIAL.
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 333 333 E -> G (IN REF. 2).
 FT CONFLICT 342 342 E -> Q (IN REF. 2).
 FT CONFLICT 388 388 P -> F (IN REF. 2).
 SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 67.4%; Score 834.5; DB 1; Length 398;
 Best Local Similarity 66.7%; Pred. No. 8e-61;
 Matches 148; Conservative 34; Mismatches 37; Indels 3; Gaps 1;

Qy 8 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 || || :|||||:||||| ||| |:||||| :||:| :||| |
 Db 106 PPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSFVVDNKE 165
 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 || | |:||| |||||:|||| | : ||||: |||:|||||:|||||:||||| ||:
 Db 166 VHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRA 225
 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDS 184
 : |||||:| |:::| :||||| |: ||||| |:| :| |||:|||||:
 Db 226 QTPQVYTIPPPREQMSKKKVSILTCLVTNFFSEAI SVEWERNGELEQDYKNTTPILDSGT 285
 Qy 185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 226

Db 286 YFLYSKLTVDTSWLQGEIFTCSVVHEALHNHHTQKNLSRSP 327

RESULT 10

GC1_RAT

ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 66.1%; Score 818.5; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 1.3e-59;
Matches 142; Conservative 41; Mismatches 35; Indels 7; Gaps 2;

Qy 7 CPPCPAPELLGG---PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 63
| | : | ||:||||| | |: ||:|||||||:| :||| |:|:| |
Db 106 CKPC----ICTGSEVSSVFIFPPKPKDVLITITLTPKVTCVVVDISQDDPEVHFSWFVDDV 161
Qy 64 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 123
||| |:|:| |||:||||: || | :|||||||:| :|||:| | |:||||||| :|:

```

ID      GC1_MOUSE          STANDARD;          PRT;          324 AA.
AC      P01868;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Ig gamma-1 chain C region secreted form.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=80045036; PubMed=115593;
RA      Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA      Takahashi N., Mano Y.;
RT      "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT      gamma 1 chain gene.";
RL      Cell 18:559-568(1979).
RN      [2]
RP      SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX      MEDLINE=80202559; PubMed=6769752;
RA      Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA      Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT      "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT      cloned in a bacterial plasmid.";
RL      Gene 9:87-97(1980).
RN      [3]
RP      SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX      MEDLINE=80012837; PubMed=113776;
RA      Rogers J., Clarke P., Salser W.;
RT      "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT      heavy chain.";
RL      Nucleic Acids Res. 6:3305-3321(1979).
RN      [4]
RP      SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX      MEDLINE=78242288; PubMed=98524;
RA      Adetugbo K.;
RT      "Evolution of immunoglobulin subclasses. Primary structure of a
RT      murine myeloma gammal chain.";
RL      J. Biol. Chem. 253:6068-6075(1978).
RN      [5]
RP      DISULFIDE BONDS (MOPC 21).
RX      MEDLINE=73008889; PubMed=5073237;
RA      Svasti J., Milstein C.;

```

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RT  "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL  Biochem. J. 126:837-850(1972).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=Secreted;
CC      IsoId=P01868-1; Sequence=Displayed;
CC      Note=May be the major isoform;
CC      Name=Membrane-bound;
CC      IsoId=P01869-1; Sequence=External;
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; V00793; CAA24172.1; -.
DR  EMBL; V00793; CAA24173.1; -.
DR  EMBL; V00793; CAA24174.1; -.
DR  EMBL; V00793; CAA24175.1; -.
DR  EMBL; V00795; CAA24176.1; -.
DR  PIR; A02159; G1MS.
DR  PDB; 1IGC; 03-JUN-95.
DR  GlycoSuiteDB; P01868; -.
DR  MGD; MGI:96446; Igh-4.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; ig; 3.
DR  SMART; SM00407; IGc1; 2.
DR  PROSITE; PS50835; IG_LIKE; 3.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW  Alternative splicing; 3D-structure.
FT  NON_TER      1      1
FT  DOMAIN        1     97      CH1.
FT  DOMAIN       98    110      HINGE.
FT  DOMAIN      111    217      CH2.
FT  DOMAIN      218    324      CH3.
FT  DISULFID      27     82
FT  DISULFID     102    102      INTERCHAIN (WITH A LIGHT CHAIN).
FT  DISULFID     104    104      INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID     107    107      INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID     109    109      INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID     138    198
FT  CARBOHYD     174    174      N-LINKED (GLCNAC. . .).
FT                                     /FTid=CAR_000055.
FT  DISULFID     244    302
FT  MOD_RES       324    324      REMOVED POST-TRANSLATIONALLY.
FT  CONFLICT      276    276      N -> D (IN REF. 3).
FT  CONFLICT      278    278      N -> D (IN REF. 3).
SQ  SEQUENCE    324 AA;  35704 MW;  A338812F3D1F2C93 CRC64;

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Query Match

66.0%; Score 817.5; DB 1; Length 324;

Best Local Similarity 62.5%; Pred. No. 1.5e-59;
Matches 140; Conservative 44; Mismatches 35; Indels 5; Gaps 2;

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Qy      7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     104 CKPCICTVPEV---SSVFIFPPKPKDVLITITLTPKVTCTVVVDISKDDPEVQFSWFVDDVE 160

Qy     65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     161 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 220

Qy     125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 184
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     221 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGS 280

Qy     185 FFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 228
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     281 YFVYSKLVNPKSNWEAGNTFTCSVLHEGLHNHTEKSLSHSPGK 324
```

RESULT 12

GC1M_MOUSE

ID GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]

RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=Displayed;
 CC Name=Secreted;
 CC IsoId=P01868-1; Sequence=External;
 CC Note=May be the major isoform;
 CC -----
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 CC -----
 DR EMBL; V00793; CAA24172.1; -.
 DR EMBL; V00793; CAA24173.1; -.
 DR EMBL; V00793; CAA24174.1; -.
 DR PIR; B02159; G1MSM.
 DR PDB; 15C8; 23-MAR-99.
 DR PDB; 1AE6; 18-MAR-98.
 DR PDB; 1CL7; 12-JAN-00.
 DR PDB; 1F11; 06-FEB-01.
 DR PDB; 1F58; 29-DEC-99.
 DR PDB; 1KC5; 24-JUL-02.
 DR PDB; 1KCR; 11-MAY-02.
 DR PDB; 25C8; 09-JUL-99.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane; 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302

FT TRANSMEM 340 357 POTENTIAL.
 FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 65.6%; Score 812.5; DB 1; Length 393;
 Best Local Similarity 62.3%; Pred. No. 4.9e-59;
 Matches 139; Conservative 44; Mismatches 35; Indels 5; Gaps 2;

Qy 7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 | | | | : | | | | | | | | | | : | | | | | | | | : | | | | | | | |
 Db 104 CKPCICTVPEV---SSVFIFPPKPKDVLITITLTPKVTCTVVVDISKDDPEVQFSWFVDDVE 160
 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 | | | : | | | | | | | | | | | | | : | | | | | | | | : | | | | | | | |
 Db 161 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 220
 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
 : | | | | : | | : : : | : | | | | : | : | | | | | | | | | | : : : : | |
 Db 221 KAPQVYTIPPPKEQMAKDVKSLTTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGS 280
 Qy 185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
 : | : | | | | | | | : | | | : | | | | | | | | | | | | | | | | | |
 Db 281 YFVYSKLVNQKSNWEAGNTFTCSVLHEGLHNHHTTEKSLSHSPG 323

RESULT 13

GCC_RAT

ID GCC_RAT STANDARD; PRT; 329 AA.
 AC P20762;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2C chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88166903; PubMed=3127222;
 RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
 RT region cDNA: extensive homology to mouse gamma 3.";
 RL Eur. J. Immunol. 18:317-319(1988).

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 CC -----

DR EMBL; X07189; CAA30169.1; -.
 DR PIR; S00847; S00847.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 222 CH2.
 FT DOMAIN 223 329 CH3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 143 203
 FT DISULFID 249 307
 SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 65.4%; Score 809.5; DB 1; Length 329;
 Best Local Similarity 63.8%; Pred. No. 6.9e-59;
 Matches 143; Conservative 41; Mismatches 37; Indels 3; Gaps 1;

Qy 8 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
 || : || ||||:||||| ||: ||:||||||| |:|:|:|:|:| |
 Db 106 PPTDICSCDDNLGRPSVFIFPPKPKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVR 165
 Qy 65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
 | |:|:| ||| | |:|||| | : ||||:||||:||||:| | |:||||||| |:|
 Db 166 VFTAQTQPHEEQNLNGTFRVVSSTLHIHQDWMMSGKEFKCKVNNKDLPSPIEKTISKPRGKA 225
 Qy 125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS 184
 | |||||:| | :||:|:|:|:|:| | ||: |:| ||| |:| | :| | ||||| |
 Db 226 RTPQVYTIPPPREQMSKNKVSITCMVTSFYPAISVFEWERNGELEQDYKNTLPVLDSDES 285
 Qy 185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 :| |||||:| | | :||:|:|:|:|:|:|:|:|:|:| | |||
 Db 286 YFLYSKLSVDTDSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK 329

RESULT 14

GCAA_MOUSE

ID GCAA_MOUSE STANDARD; PRT; 330 AA.
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2A chain C region, A allele.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;

RT "Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RT sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Ollo R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE=74175517; PubMed=4831970;
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a
 RT immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462(1972).
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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 CC -----
 DR EMBL; V00798; CAA24178.1; -.
 DR PIR; A02152; G2MSA.
 DR PDB; 1E4W; 12-JUL-01.
 DR PDB; 1E4X; 12-JUL-01.
 DR PDB; 1MNU; 06-MAY-99.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.

FT	NON_TER	1	1	
FT	DOMAIN	6	98	IG-LIKE 1.
FT	DOMAIN	121	220	IG-LIKE 2.
FT	DOMAIN	229	325	IG-LIKE 3.
FT	DISULFID	15	15	INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID	27	82	
FT	DISULFID	107	107	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	110	110	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	112	112	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	MOD_RES	330	330	REMOVED POST-TRANSLATIONALLY.
SQ	SEQUENCE	330 AA;	36389 MW;	B84361C5445A6864 CRC64;

Query Match 65.3%; Score 809; DB 1; Length 330;
 Best Local Similarity 65.2%; Pred. No. 7.6e-59;
 Matches 146; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

Qy	7	CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE	64
		: : : :	
Db	107	CPPCKCPAPNLLGGPSVFIFPPKIKDVLMLSLSPIVTCVVVDVSEDDPDVQISWFWNNVE	166
Qy	65	VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP	124
		: : : : : :	
Db	167	VHTAQTQTHREDYNSTLRVVSALPIQHQQWMSGKEFKCKVNNKDLPAPIERTISKPKGSV	226
Qy	125	REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS	184
		: : : :	
Db	227	RAPQVYVLPPEEEMTKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS	286
Qy	185	FFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK	228
		: : : : : : :	
Db	287	YFMYSKLRVEKKNWVERNSYSCSVHEGLHNHHTTKSFSRTPGK	330

RESULT 15

GCAM_MOUSE

ID GCAM_MOUSE STANDARD; PRT; 399 AA.
 AC P01865;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2A chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Membrane-bound;

```

CC      IsoId=P01865-1; Sequence=Displayed;
CC      Name=Secreted;
CC      IsoId=P01864-1; Sequence=External;
CC      Note=Probably the major isoform;
CC      -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC      -----
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CC      -----
DR      EMBL; J00471; AAB59661.1; ALT_INIT.
DR      PIR; A02154; G2MSAM.
DR      PDB; 1KB5; 08-APR-98.
DR      PDB; 1YEE; 15-OCT-97.
DR      MGD; MGI:96443; Igh-1.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 2.
DR      SMART; SM00407; IGc1; 2.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW      Transmembrane; Alternative splicing; 3D-structure; Repeat.
FT      NON_TER      1      1
FT      DOMAIN      6      98      IG-LIKE 1.
FT      DOMAIN      121     220     IG-LIKE 2.
FT      DOMAIN      229     325     IG-LIKE 3.
FT      DISULFID      15      15      INTERCHAIN (WITH A LIGHT CHAIN).
FT      DISULFID      27      82
FT      DISULFID      107     107     INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      110     110     INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      112     112     INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      144     204
FT      DISULFID      250     308
FT      TRANSMEM      346     363      POTENTIAL.
FT      DOMAIN      364     399      CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD      180     180      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

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Query Match      64.9%; Score 804; DB 1; Length 399;
Best Local Similarity 65.0%; Pred. No. 2.5e-58;
Matches 145; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

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Qy      7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64
      ||| ||| |||||:|||| || |||| :| ||||| ||| :||:|: :|:|: ||
Db      107 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMI SLSPIVTCVVVDVSEDDPDVQISWFWNNVE 166

Qy      65 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
      || |:|: | ||| ||| | : |||:| |||:| |||:| |||:| ||| ||
Db      167 VHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLPAPIERTISKPKGSV 226

Qy      125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 184

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Db	227	RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS	286
Qy	185	FFLYSKLTVDKSRWQQGNVFSVHEALHNHYTQKSLSLSPG	227
Db	287	YFMYSKLRVEKKNWVERNSYSCSVHEGLHNHHTTKSFSRTPG	329

Search completed: January 16, 2004, 09:36:59
Job time : 18 secs